



## SEQUENCE LISTING

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<110> Benjanin, Stephane  
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US4.DIV

<140> US 09/992,600

<141> 2001-11-13

<150> US 09/924,340

<151> 2001-08-06

<150> PCT/IB01/01715

<151> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

<151> 2001-06-15

<150> US 60/293,574

<151> 2001-05-25

<160> 114

<170> JPatent

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 Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser Thr  
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 gac cac acc aaa atg cca tct caa atg gaa cac gcc atg gaa acc atg 1581  
 Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met  
 35 40 45  
 atg ttt aca ttt cac aaa ttc gct ggg gat aaa ggc tac tta aca aag 1629  
 Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr Lys  
 50 55 60 65  
 gag gac ctg aga gta ctc atg gaa aag gag ttc cct gga ttt ttg gaa 1677  
 Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu Glu  
 70 75 80  
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 Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp  
 85 90 95  
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 Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu Ile  
 100 105 110  
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 Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys  
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Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val	
80 85 90	
ggc act ggg ttc agt tat gtg aat ggt agt ggt gcc tat gcc aag gac	440
Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp	
95 100 105	
ctg gct atg gtg gct tca gac atg atg gtt ctc ctg aag acc ttc ttc	488
Leu Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe	
110 115 120 125	
agt tgc cac aaa gaa ttc cag aca gtt cca ttc tac att ttc tca gag	536
Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu	
130 135 140	
tcc tat gga gga aaa atg gca gct ggc att ggt cta gag ctt tat aag	584
Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys	
145 150 155	
gcc att cag cga ggg acc atc aag tgc aac ttt gcg ggg gtt gcc ttg	632
Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu	
160 165 170	
ggt gat tcc tgg atc tcc cct gtt gat tgc gtg ctc tcc tgg gga cct	680
Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro	
175 180 185	
tac ctg tac agc atg tct ctt ctc gaa gac aaa ggt ctg gca gag gtg	728
Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys Gly Leu Ala Glu Val	
190 195 200 205	
tct aag gtt gca gag caa gta ctg aat gcc gta aat aag ggg ctc tac	776
Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr	
210 215 220	
aga gag gcc aca gag ctg tgg ggg aaa gca gaa atg atc att gaa cag	824
Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln	
225 230 235	
gta aaa agg gga aac act cag agg cta gcc tgc ttg gct ttt tct ggt	872
Val Lys Arg Gly Asn Thr Gln Arg Leu Ala Cys Leu Ala Phe Ser Gly	
240 245 250	
ggg tac agg gcc cat ggt tgg tgt tgt caa act tgg agt cta cac	917
Gly Tyr Arg Ala His Gly Trp Cys Cys Gln Thr Trp Ser Leu His	
255 260 265	
tgaggctccc cacatatctg caaatgattg catgctggat aataaatctc ttgggtctaa	977
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-10 -5 1 5	
Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp	
10 15 20	
Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn	
25 30 35	
Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly	
40 45 50	
Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser	
55 60 65 70	
Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu	





Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu  
 25 30 35 40  
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 Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe  
 45 50 55  
 tca att gtc act tgatgatata attgcaattt aaactgttaa gctgtgttca 357  
 Ser Ile Val Thr  
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 taaataaaaa a 438

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 Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe  
 15 20 25  
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Met	Thr	Gln	Ser	Pro	Leu	Phe	Leu
5				10			15
tcc	atc	tcc	tgc	agg	tct	agt	cag
Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln
			25				30
aac	tat	ttg	gat	tgg	tac	cac	cag
Asn	Tyr	Leu	Asp	Trp	Tyr	His	Gln
		40					45
ctg	ata	tac	ttg	ggt	tct	aat	cgg
Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg
		55					60
agt	ggc	agt	gga	tca	ggc	aca	gat
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
	70					75	
gag	gct	gag	gat	gtt	ggg	gtt	tat
Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr
85				90			95
cca	ttc	act	ttc	ggc	cct	ggg	acc
Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr
			105				110
gct	gca	cca	tct	gtc	ttc	atc	ttc
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe
		120					125
tct	gga	act	gcc	tct	gtt	gtg	tgc
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys
	135						140
gag	gcc	aaa	gta	cag	tgg	aag	gtg
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val
	150					155	
tcc	cag	gag	agt	gtc	aca	gag	cag
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln
165				170			175
ctc	agc	agc	acc	ctg	acg	ctg	agc
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser
			185				190
gtc	tac	gcc	tgc	gaa	gtc	acc	cat
Val	Tyr	Ala	Cys	Glu	Val	Thr	His
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aag	agc	ttc	aac	agg	gga	gag	tgt
Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys
	215					220	
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 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser



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Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
65 70 75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
80 85 90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
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20 25 30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35 40 45 50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
55 60 65
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70 75 80
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gccctcaggc ctcaggcctt ccttggtctg aagattgggc ttcacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
-10 -5
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
1 5 10 15

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ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
      35      40      45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
      50      55      60
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Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65      70      75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80      85      90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
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Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20      25      30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35      40      45      50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
      55      60      65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
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Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
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gccctcaggc ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccct 240  
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289

Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala

-10

-5

aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337  
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly

1

5

10

15

atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385  
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys

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ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433  
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys

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tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481  
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser

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ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529  
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70

75

agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574  
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser

80 tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634  
ctttgaaatg taggtagctt attatccaca ttttgcatg gaggaacag agtcaggtga 694  
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-10

-5

1

Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile

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Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser

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Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg

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Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp

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Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser

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Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser

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 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccctt 240  
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 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337  
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly  
 1 5 10 15  
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385  
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys  
 20 25 30  
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433  
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys  
 35 40 45  
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481  
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser  
 50 55 60  
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529  
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu  
 65 70 75  
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574  
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser  
 80 85 90  
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 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg  
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 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp  
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 taggactttt cccatccaat tttgtaacaa ctaatttaaa catagagact gaggcagcgg 240  
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 agcctgttta tatagatgag gataag atg gat aga gcc ctg cag gta ctt cag 353  
 Met Asp Arg Ala Leu Gln Val Leu Gln  
 1 5  
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 Ser Ile Asp Pro Thr Asp Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp  
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 Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu  
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 Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys  
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 Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro  
 75 80 85  
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 Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly  
 90 95 100 105  
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 Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser  
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 Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro  
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 aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta 785  
 Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu  
 140 145 150  
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 Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn  
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Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met	
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Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu	
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Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu	
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Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu	
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Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys	
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Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met	
85 90 95	
Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser	
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Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln	
115 120 125	
Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr	
130 135 140	
Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val	
145 150 155 160	
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Met Arg
-15
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Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala
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Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr
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Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val
20 25 30
gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg 309
Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val
35 40 45 50
gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc aag gtg 357
Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val
55 60 65
tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc 405
Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro
70 75 80
acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat 453
Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn
85 90 95
gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc 501
Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys
100 105 110
acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc 549
Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile
115 120 125 130
ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa 597
Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu
135 140 145
ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg 645
Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu
150 155 160
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Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu
165 170 175
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Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp
180 185 190
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His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg
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Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr	
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Val Ile Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala	
45 50 55 60	
ata aca cca tta cct ccc aag aaa gaa aat gat gaa atg ccc acg tgt	408
Ile Thr Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys	
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ctg ctg tgt gtt tgt tta agt ggc tct gta tac tgt gaa gaa gtt gac	456
Leu Leu Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp	
80 85 90	
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Ile Asp Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala	
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Arg Phe Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile	
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cct aac tta aga aga ctc gat ttt aca gga aat ttg ata gaa gat ata	600
Pro Asn Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile	
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Glu Asp Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu	
145 150 155	
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Ala Glu Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr	
160 165 170	
tta ttt aat gca aaa tac aac aaa atc aag agt agg gga atc aaa gca	744
Leu Phe Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala	
175 180 185	
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Asn Ala Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His	
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aat gcc ctg gaa tcc gtg cct ctt aat tta cca gaa agt cta cgt gta	840
Asn Ala Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val	
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Ile His Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe	
225 230 235	
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Cys Lys Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile	
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Arg Leu Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe	
255 260 265	
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Ile Cys Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe	
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 ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta 147  
 Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val  
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 Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala  
 35 40 45  
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 Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly  
 50 55 60  
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 Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro  
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 Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu  
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 Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu  
 145 150 155  
 aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt 579  
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 160 165 170  
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 Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val  
 175 180 185 190  
 aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc 675  
 Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe  
 195 200 205  
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 Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp  
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Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
240 245 250
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca 867
Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
255 260 265 270
cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc 915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
275 280 285
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc 963
Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
290 295 300
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320 325 330
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Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
335 340 345 350
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370 375 380
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Leu Leu Lys
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 Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr  
 35 40 45  
 Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu  
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Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu
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Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu
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Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr
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Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met
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Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr
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Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser
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Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu
			195						200				205		
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile
		210					215					220			
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser
		225				230					235				
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp
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Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser
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Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val
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Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys
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His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val
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Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu
320					325					330					335
Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala	Leu
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Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu	Arg
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gccaggagag tccccacagg agtgtcaggt ttcaatctca gcaccagcca ctgagagcag 120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc 168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
            -20                    -15                    -10
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca 216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
            -5                    1                    5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca 264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
            10                    15                    20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat 312
Ala Arg Asn Ser Tyr His Gln Ile His Lys Asn Gly His Val Asp
            25                    30                    35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag 360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
            40                    45                    50                    55
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc 408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
            60                    65                    70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg 456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
            75                    80                    85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc 504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
            90                    95                    100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag 552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
            105                    110                    115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg 600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Tyr Ser Gln Phe Leu
            120                    125                    130                    135
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca 648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
            140                    145                    150
cgg cgg cac acc cgg agc gcc gag gac gac tgg gag cgg gac ccc ctg 696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
            155                    160                    165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt 744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
            170                    175                    180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac 792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
            185                    190                    195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga 840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
            200                    205                    210                    215
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggtcgct 889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
            220                    225
ggaagggcac cctctttaac ccattccctca gcaaacgcag ctcttcccaa ggaccaggtc 949
ccttgacgtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct 1009
gggggtccctt ccacaggagg tcctgtgaga accaaccctt gaggcccaag tcatgggggt 1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa 1129
ctagaaattt ccccttcatg aaggtagaga gaaggggtct ctcccaacat atttctcttc 1189
cttggtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa 1239

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<210> 26
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<212> PRT
<213> Homo sapiens

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 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu  
                   -5                  1                  5  
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg  
       10                  15                  20  
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala  
 25                  30                  35                  40  
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala  
                   45                  50                  55  
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met  
                   60                  65                  70  
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn  
                   75                  80                  85  
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His  
       90                  95                  100  
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala  
 105                  110                  115                  120  
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg  
                   125                  130                  135  
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg  
                   140                  145                  150  
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val  
                   155                  160                  165  
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln  
       170                  175                  180  
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu  
 185                  190                  195                  200  
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly  
                   205                  210                  215  
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile  
                   220                  225

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 <212> DNA  
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<220>  
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 <222> 1164..1179

<220>  
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 <222> 116  
 <223> Xaa = Asn,Thr

<220>  
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 <223> Xaa = Phe,Ser

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 tgggtctctg actcacttct gacttttaggc gctcgaggac tgtgcccagg agcag atg 118  
 Met  
 1  
 cgg ctc aga gcc cag gtg cgc ctg ctt gag acc cgg gtc aaa cag caa 166  
 Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln  
 5 10 15  
 cag gtc aag atc aag cag ctt ttg cag gag aat gaa gtc cag ttc ctt 214  
 Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu  
 20 25 30  
 gat aaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag 262  
 Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln  
 35 40 45  
 tat gca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga 310  
 Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly  
 50 55 60 65  
 ttt tac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat 358  
 Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr  
 70 75 80  
 tgt gac atg tcc gat gga gga gga tgg act gta att cag aga cga tct 406  
 Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg Ser  
 85 90 95  
 gat ggc agt gaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc 454  
 Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly  
 100 105 110  
 ttt gga amt ttt gtc caa aaa cat ggt gaa tat tgg ctg ggc aat aaa 502  
 Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys  
 115 120 125  
 aat ctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac 550  
 Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp  
 130 135 140 145  
 ctt gca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc 598  
 Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe  
 150 155 160  
 aaa gtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat 646  
 Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr  
 165 170 175  
 tct gga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg 694  
 Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val  
 180 185 190  
 cag tgg tgg gct agt cac caa aga atg aaa ttc agc acg tgg gac aga 742  
 Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg  
 195 200 205  
 gat cat gac aac tat gaa ggg aac tgc gca gaa gaa gat cag tct ggc 790  
 Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly  
 210 215 220 225  
 tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac 838  
 Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr  
 230 235 240  
 agc ggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc 886  
 Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr  
 245 250 255

tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg 934  
 Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg  
 260 265 270  
 cca aat gat ttt att cca aat gta att taattgctgc tggtgggctt 981  
 Pro Asn Asp Phe Ile Pro Asn Val Ile  
 275 280  
 tcgtttctgc aattcagctt tgtttaaagt gatttgaaaa atactcattc tgaacatatc 1041  
 catgcgcaat catgataact gttgtgagta gtgcttttca ttcttctcac ttgcctttgt 1101  
 tacttaatgt gctttcagta cagcagatat gcaatattca ccaaataaat gtagactgtg 1161  
 tcaaaaaaaaa aaaaaaaaa 1179

<210> 28  
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 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> 116  
 <223> Xaa = Asn,Thr

<220>  
 <221> UNSURE  
 <222> 233  
 <223> Xaa = Phe,Ser

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 Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe  
 20 25 30  
 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg  
 35 40 45  
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser  
 50 55 60  
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val  
 65 70 75 80  
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg  
 85 90 95  
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn  
 100 105 110  
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn  
 115 120 125  
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile  
 130 135 140  
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn  
 145 150 155 160  
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu  
 165 170 175  
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu  
 180 185 190  
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp  
 195 200 205  
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser  
 210 215 220  
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr  
 225 230 235 240  
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr  
 245 250 255  
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile  
 260 265 270  
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile  
 275 280

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 <213> Homo sapiens

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 <222> 1..344

<220>  
 <221> CDS  
 <222> 345..1118

<220>  
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 <222> 1103..1118

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 tgtggcctgg gggaaggagg acgaggttct gcctggatcc cagcaggacg ctgtgccatt 120  
 tggaacaaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtcc 180  
 aacccttgga gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240  
 cggcccgag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300  
 agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356  
 Met Gly Arg Thr  
 cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404  
 Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala  
 -15 -10 -5 1  
 tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452  
 Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys  
 5 10 15  
 atc tgg gac gaa gac gag gag tct acg gac acc tca gag att ggg gtt 500  
 Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Glu Ile Gly Val  
 20 25 30  
 gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548  
 Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala  
 35 40 45  
 aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596  
 Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu  
 50 55 60 65  
 gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644  
 Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser  
 70 75 80  
 gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692  
 Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys  
 85 90 95  
 gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740  
 Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile  
 100 105 110  
 tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788  
 Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg  
 115 120 125  
 ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836  
 Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg  
 130 135 140 145  
 gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884  
 Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala  
 150 155 160  
 cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932  
 Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr  
 165 170 175  
 aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980

Lys	Ile	Asp	Asp	Ile	Leu	Ser	Ala	Pro	Asp	Leu	Gln	Lys	Val	Leu	Asn	
		180					185					190				
atc	ctg	gag	cga	aca	aat	gat	cct	ttt	att	caa	gaa	gta	gcc	ttg	gtc	1028
Ile	Leu	Glu	Arg	Thr	Asn	Asp	Pro	Phe	Ile	Gln	Glu	Val	Ala	Leu	Val	
		195				200					205					
act	ctg	ggt	aac	aat	gca	gca	tat	tca	ttt	aac	cag	aat	gcc	ata	cgt	1076
Thr	Leu	Gly	Asn	Asn	Ala	Ala	Tyr	Ser	Phe	Asn	Gln	Asn	Ala	Ile	Arg	
210					215					220					225	
gaa	ttg	ggt	ggt	gtc	cca	att	att	gca	aaa	aaa	aaa	aaa	aaa			1118
Glu	Leu	Gly	Gly	Val	Pro	Ile	Ile	Ala	Lys	Lys	Lys	Lys	Lys			
				230					235							

<210> 30  
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 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> 1..20

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Met	Gly	Arg	Thr	Arg	Glu	Ala	Gly	Cys	Val	Ala	Ala	Gly	Val	Val	Ile	
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Gly	Ala	Gly	Ala	Cys	Tyr	Cys	Val	Tyr	Arg	Leu	Ala	Trp	Gly	Arg	Asp	
				1				5					10			
Glu	Asn	Glu	Lys	Ile	Trp	Asp	Glu	Asp	Glu	Glu	Ser	Thr	Asp	Thr	Ser	
		15				20						25				
Glu	Ile	Gly	Val	Glu	Thr	Val	Lys	Gly	Ala	Lys	Thr	Asn	Ala	Gly	Ala	
30					35					40						
Gly	Ser	Gly	Ala	Lys	Leu	Gln	Gly	Asp	Ser	Glu	Val	Lys	Pro	Glu	Val	
45					50					55					60	
Ser	Leu	Gly	Leu	Glu	Asp	Cys	Pro	Gly	Val	Lys	Glu	Lys	Ala	His	Ser	
				65				70						75		
Gly	Ser	His	Ser	Gly	Gly	Gly	Leu	Glu	Ala	Lys	Ala	Lys	Ala	Leu	Phe	
			80					85						90		
Asn	Thr	Leu	Lys	Glu	Gln	Ala	Ser	Ala	Lys	Ala	Gly	Lys	Gly	Ala	Arg	
		95				100						105				
Val	Gly	Thr	Ile	Ser	Gly	Asn	Arg	Thr	Leu	Ala	Pro	Ser	Leu	Pro	Cys	
110						115					120					
Pro	Gly	Gly	Arg	Gly	Gly	Cys	His	Pro	Thr	Arg	Ser	Gly	Ser	Arg		
125					130					135				140		
Ala	Gly	Gly	Arg	Ala	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Ala	Arg	Ser	Lys	
				145					150					155		
Ser	Thr	Arg	Ala	Pro	Ala	Thr	Thr	Trp	Pro	Val	Arg	Arg	Gly	Lys	Phe	
			160					165					170			
Asn	Phe	Pro	Tyr	Lys	Ile	Asp	Asp	Ile	Leu	Ser	Ala	Pro	Asp	Leu	Gln	
		175				180						185				
Lys	Val	Leu	Asn	Ile	Leu	Glu	Arg	Thr	Asn	Asp	Pro	Phe	Ile	Gln	Glu	
190						195					200					
Val	Ala	Leu	Val	Thr	Leu	Gly	Asn	Asn	Ala	Ala	Tyr	Ser	Phe	Asn	Gln	
205					210					215					220	
Asn	Ala	Ile	Arg	Glu	Leu	Gly	Gly	Val	Pro	Ile	Ile	Ala	Lys	Lys	Lys	
				225					230					235		

Lys Lys

<210> 31  
 <211> 1273  
 <212> DNA  
 <213> Homo sapiens

<220>  
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<222> 1..13

<220>

<221> CDS

<222> 14..1048

<220>

<221> 3'UTR

<222> 1049..1273

<220>

<221> polyA\_signal

<222> 1234..1239

<220>

<221> polyA\_site

<222> 1258..1273

<400> 31

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tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag      97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
          -10                      -5                      1

ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac     145
Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn
          5                      10                      15

ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt     193
Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val
          20                      25                      30                      35

gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga     241
Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg
          40                      45                      50

agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc     289
Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro
          55                      60                      65

tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt     337
Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe
          70                      75                      80

aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg     385
Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu
          85                      90                      95

aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg     433
Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu
          100                      105                      110                      115

gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac     481
Asp Ser Ile Arg Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn
          120                      125                      130

aag tgg tgg aat aac cta agt gat ggc cag cgg act gtg aca ggt att     529
Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile
          135                      140                      145

ata gct gca aat gtc ctt gta ttc tgt tta tgg aga gta cct tct ctg     577
Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu
          150                      155                      160

cag cgg aca atg atc aga tat ttc aca tcg aat cca gcc tca aag gtc     625
Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val
          165                      170                      175

ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt     673
Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe
          180                      185                      190                      195

cac atg gca gca aat atg tat gtt ttg tgg agc ttc tct tcc agc ata     721
His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile
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	200		205		210	
gtg aac att ctg ggt caa gag cag ttc atg gca gtg tac cta tct gca						769
Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala						
	215		220		225	
ggg gtt att tcc aat ttt gtc agt tac gtg ggt aaa gtt gcc aca gga						817
Gly Val Ile Ser Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly						
	230		235		240	
aga tat gga cca tca ctt ggt gca gcc ctg aaa gcc att atc gcc atg						865
Arg Tyr Gly Pro Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met						
	245		250		255	
gat aca gca gga atg atc ctg gga tgg aaa ttt ttt gat cat gcg gca						913
Asp Thr Ala Gly Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala						
	260		265		270	275
cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat						961
His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His						
	280		285		290	
gaa ctg att tgg aag aac agg gag ccg cta gtg aaa atc tgg cat gaa						1009
Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu						
	295		300		305	
ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg						1058
Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Gly Ser Lys						
	310		315		320	
attggacagt agtgggtgcat ctgggtccttg ccgcctgaga gcccaggag acatcggcta						1118
gagtgaccat ggctatgctc ccgtctggaa gatgccagca tctggcctcc cacttttttc						1178
agctgtgtcc ccagtcctgt gtcttttttag aatgtgaatg atgataaagt tgtgaaataa						1238
aggtttctat ctagtttgca aaaaaaaaaa aaaaaa						1273

<210> 32

<211> 345

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..26

<400> 32

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-25		-20			-15	
Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val						
-10		-5		1		5
Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln						
	10		15			20
Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg						
	25		30		35	
Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile						
	40		45		50	
Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg						
55		60		65		70
Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala						
	75		80			85
Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val						
	90		95			100
Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg						
	105		110		115	
Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn						
	120		125		130	
Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn						
135		140		145		150
Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met						
	155		160			165
Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro						
	170		175			180

Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala  
185 190 195  
Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu  
200 205 210  
Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser  
215 220 225 230  
Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro  
235 240 245  
Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly  
250 255 260  
Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly  
265 270 275  
Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp  
280 285 290  
Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn  
295 300 305 310  
Gly Pro Lys Lys Gly Gly Gly Ser Lys  
315

<210> 33  
<211> 723  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> 1..72

<220>  
<221> CDS  
<222> 73..672

<220>  
<221> 3'UTR  
<222> 673..723

<220>  
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<222> 689..694

<220>  
<221> polyA\_site  
<222> 708..723

<400> 33  
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accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111  
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val  
1 5 10  
ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159  
Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser  
15 20 25  
gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207  
Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg  
30 35 40 45  
aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255  
Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr  
50 55 60  
ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303  
Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro  
65 70 75  
agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351  
Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val

80	85	90	
ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc			399
Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr			
95	100	105	
aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc			447
Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala			
110	115	120	125
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta			495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu			
130	135	140	
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag			543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys			
145	150	155	
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc			591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe			
160	165	170	
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc			639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys			
175	180	185	
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata			692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys			
190	195	200	
aagatgtgtt aaaataaaaa aaaaaaaaaa t			723

<210> 34  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

<400> 34	
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	20 25 30
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys	
	35 40 45
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe	
	50 55 60
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro	
65	70 75 80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile	
	85 90 95
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr	
	100 105 110
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala	
	115 120 125
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn	
	130 135 140
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr	
145	150 155 160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile	
	165 170 175
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu	
	180 185 190
Asp Cys Asp Cys Glu Gln Cys Cys	
195	200

<210> 35  
 <211> 845  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> 5'UTR  
 <222> 1..118

<220>  
 <221> CDS  
 <222> 119..655

<220>  
 <221> 3'UTR  
 <222> 656..845

<220>  
 <221> polyA\_signal  
 <222> 809..814

<220>  
 <221> polyA\_site  
 <222> 830..845

<400> 35  
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 taaattctgc caaaaggact gaggaacggt gcctggaaaaa gggcaagaat atcacggc 118  
 atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166  
 Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe  
 1 5 10 15  
 aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214  
 Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile  
 20 25 30  
 tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262  
 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro  
 35 40 45  
 tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310  
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met  
 50 55 60  
 gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358  
 Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys  
 65 70 75 80  
 ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406  
 Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu  
 85 90 95  
 gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454  
 Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser  
 100 105 110  
 atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502  
 Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser  
 115 120 125  
 atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550  
 Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp  
 130 135 140  
 acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598  
 Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly  
 145 150 155 160  
 tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646  
 Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg  
 165 170 175  
 ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695  
 Gly Pro Tyr  
 atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctgggt 755  
 attatctctc tatcagataa gattttgtta atgtactatt ttactcttca ataaataaaa 815  
 cagtttatta tcgcaaaaaa aaaaaaaaaa 845

<210> 36  
 <211> 179

<212> PRT

<213> Homo sapiens

<400> 36

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20          25          30
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35          40          45
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50          55          60
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65          70          75          80
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85          90          95
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100         105         110
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115         120         125
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130         135         140
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145         150         155         160
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165         170         175
Gly Pro Tyr
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<210> 37

<211> 517

<212> DNA

<213> Homo sapiens

<220>

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<222> 1..16

<220>

<221> CDS

<222> 17..259

<220>

<221> 3'UTR

<222> 260..517

<400> 37

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          Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu
          1          5          10
gcc ctg tgg gtg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100
Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu
15          20          25
gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148
Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu
30          35          40
gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196
Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser
45          50          55          60
aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244
Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp
65          70          75
gga caa gaa ata gcc tgaccatgag gaccaggagg ctgctacccc tcctacagc 299
Gly Gln Glu Ile Ala
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80  
tcttaccctc tggctgcaat ggggctgcac tgtgagccct gcccccaaca gatgcctcct 359  
gctctgacag gtgggctcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419  
tttctccaat ggacatgatt cccaagtcac cctgctgcct tttttcttat agacacaatg 479  
aacagaccac ccacaacctt agttctctaa gtcctcct 517

<210> 38  
<211> 81  
<212> PRT  
<213> Homo sapiens

<400> 38  
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Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala  
20 25 30  
Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala  
35 40 45  
Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu  
50 55 60  
Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile  
65 70 75 80  
Ala

<210> 39  
<211> 1816  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> 1..259

<220>  
<221> CDS  
<222> 260..1048

<220>  
<221> 3'UTR  
<222> 1049..1816

<220>  
<221> polyA\_signal  
<222> 1782..1787

<220>  
<221> polyA\_site  
<222> 1801..1816

<400> 39  
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ggaacctcgg gagcggcagc tccggcgccct ggtagcgaga ggcggggtcc ggagatcccg 120  
gcctcaacttc gtcccactgt ggtaggggt gagtcctgcg aatgttaagt gatttgctca 180  
aggtgcccac ttgcaggaat ttggagccca ggccagttct ctgagcctat cattagggtc 240  
aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292  
Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu  
-15 -10  
ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340  
Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp  
-5 1 5  
atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388  
Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met  
10 15 20

ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat	436
Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr	
25 30 35 40	
gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tgc tgg gtg ggg ccc	484
Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro	
45 50 55	
aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc	532
Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe	
60 65 70	
gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat	580
Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His	
75 80 85	
gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc	628
Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr	
90 95 100	
act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc	676
Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe	
105 110 115 120	
ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc	724
Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile	
125 130 135	
cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc	772
His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val	
140 145 150	
att tgc ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc	820
Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr	
155 160 165	
agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc	868
Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr	
170 175 180	
ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg	916
Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu	
185 190 195 200	
gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag	964
Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln	
205 210 215	
ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac	1012
Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr	
220 225 230	
gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgctc	1058
Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp	
235 240	
tccaagaac agagcctgtc ccagatgtc ccagtagcga tgagtaacag aggtggctgt	1118
ggacttcctc tacttctcct tgctggatca gggccttctc gcctcccgct gggcaggtct	1178
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tgatgcaaaa gttgtggtgt ccagtgtgca gcagccctgg gagccactgc caccttcaga	1298
gggggttcctt gctgagaccc acattgcttc acctggcccc accatggctg cttgcctggc	1358
ccaacctagc gttctgtgcc atgctagaac ttgagctgtt gctcttcttc aggggaggaa	1418
atagggtgga gagcggaag ggtcttgctc ctaagtgttg ctgctgtggc ttttttgct	1478
tctccaaaga cgcactgcca ggtccaagc ttcagactgc tgtgcttagt aagcaagtga	1538
gaagcctggg gtttgagacc cacctactct ctggcagcat cagcctccta ctctggcaa	1598
catcaggcca acgtccaccc cagcctcaca ttgccagatg ttggcagaag ggctaatt	1658
gaccgtcttg actggctgga gccttcaaag ccaactgggat gtcctccagg cacctgggtc	1718
ccatgaccag ctccccgtct ccataggggt aggcatttca ctgggttatg aagctcgagt	1778
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<210> 40  
 <211> 263  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

<222> 1..20

<400> 40

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1 5 10  
Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro  
15 20 25  
Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu  
30 35 40  
Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys  
45 50 55 60  
Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val  
65 70 75  
Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn  
80 85 90  
Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe  
95 100 105  
Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala  
110 115 120  
Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly  
125 130 135 140  
Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn  
145 150 155  
Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser  
160 165 170  
Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val  
175 180 185  
Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys  
190 195 200  
Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Leu Gln Leu  
205 210 215 220  
Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly  
225 230 235  
Arg Gln Pro Tyr Lys Ser Trp  
240

<210> 41

<211> 643

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..90

<220>

<221> CDS

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<222> 463..643

<220>

<221> polyA\_signal

<222> 607..612

<220>

<221> polyA\_site

<222> 628..643



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 Met Pro Ala Cys Arg Leu Gly Pro  
 -25  
 cta gcc gcc gcc ctc ctc ctc agc ctg ctg ctg ttc ggc ttc acc cta 162  
 Leu Ala Ala Ala Leu Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu  
 -20 -15 -10  
 gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210  
 Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln  
 -5 1 5 10  
 gct gac cag aac tgc acg caa gag tgc gtc tcg gac agc gaa tgc gcc 258  
 Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala  
 15 20 25  
 gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306  
 Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu  
 30 35 40  
 ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354  
 Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro  
 45 50 55  
 cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402  
 Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro  
 60 65 70 75  
 ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450  
 Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val  
 80 85 90  
 act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502  
 Thr Pro Asn Phe  
 95  
 agttttctgcc tggccctgca tctgggttcca gcccacctgc cctcccccttt ttcgggactc 562  
 tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622  
 tcagcaaaaa aaaaaaaaaa a 643

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 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..30

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 -10 -5 1  
 Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu  
 5 10 15  
 Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala  
 20 25 30  
 Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys  
 35 40 45 50  
 Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln  
 55 60 65  
 Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn  
 70 75 80  
 Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe  
 85 90

<210> 43  
 <211> 501  
 <212> DNA

<213> Homo sapiens

<220>

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<222> 1..227

<220>

<221> CDS

<222> 228..501

<400> 43

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ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
                                     Met Gln Gly
                                     -30
act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
                                     -25
aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
                                     -10
aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
                                     5
cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
                                     20
gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
                                     40
gtt cct ttc tcc gaa ctg aaa gac a 501
Val Pro Phe Ser Glu Leu Lys Asp
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<210> 44

<211> 91

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..33

<400> 44

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                                     -30
Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Leu
                                     -15
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
                                     1
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
                                     20
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
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Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
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<210> 45

<211> 960

<212> DNA

<213> Homo sapiens

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<220>  
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 <222> 98..934

<220>  
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 <222> 935..960

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 cggcccgttt caccocgagg aggaaggaca ctgggtc atg acg cca tca gaa ggc 115  
 Met Thr Pro Ser Glu Gly  
 1 5  
 gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163  
 Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu  
 10 15 20  
 gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg 211  
 Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly  
 25 30 35  
 cgc agt ctc ttg aag gcg ctt gtc aag aaa tct gca ctg tgt ggg gag 259  
 Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu  
 40 45 50  
 caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307  
 Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu  
 55 60 65 70  
 ggt ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355  
 Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe  
 75 80 85  
 aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403  
 Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly  
 90 95 100  
 ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct 451  
 Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro  
 105 110 115  
 gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc 499  
 Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Leu Arg Leu Pro  
 120 125 130  
 tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct 547  
 Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser  
 135 140 145 150  
 tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg 595  
 Cys Pro Gly Asp Ser Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu  
 155 160 165  
 cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc 643  
 Leu His Glu Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser  
 170 175 180  
 ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg 691  
 Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser  
 185 190 195  
 gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act 739  
 Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr  
 200 205 210  
 cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg 787  
 Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly  
 215 220 225 230  
 ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccg gta 835  
 Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Pro Val  
 235 240 245

tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt	883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly	
250 255 260	
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga	931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly	
265 270 275	
ttc tagggatggg gcagagtggc agcatc	960
Phe	

<210> 46  
 <211> 279  
 <212> PRT  
 <213> Homo sapiens

<400> 46

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Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys	
35 40 45	
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser	
50 55 60	
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu	
65 70 75 80	
Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu	
85 90 95	
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys	
100 105 110	
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp	
115 120 125	
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala	
130 135 140	
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys	
145 150 155 160	
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro	
165 170 175	
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly	
180 185 190	
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln	
195 200 205	
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser	
210 215 220	
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp	
225 230 235 240	
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys	
245 250 255	
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly	
260 265 270	
Trp Gly Trp Gly Gln Gly Phe	
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<210> 47  
 <211> 1294  
 <212> DNA  
 <213> Homo sapiens

<220>  
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<220>  
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<222> 267..1139

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<221> 3'UTR

<222> 1140..1294

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<221> polyA\_signal

<222> 1246..1251

<220>

<221> polyA\_site

<222> 1279..1294

<400> 47

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ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
ttcaatacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240
gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
                                Met Ile Tyr Thr Met Lys Lys Val His
                                -25                                -20
gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
Ala Leu Trp Ala Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro
                                -15                                -10                                -5
ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
                                1                                5                                10
acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
15                                20                                25                                30
gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485
Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
                                35                                40                                45
att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
                                50                                55                                60
aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
                                65                                70                                75
aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
80                                85                                90
cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys
95                                100                                105                                110
gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725
Glu Arg Phe Lys Tyr Gly Gly Cys Leu Asn Met Asn Asn Phe Glu
                                115                                120                                125
aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773
Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe
                                130                                135                                140
cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg 821
Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu
145                                150                                155
act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869
Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro
160                                165                                170
tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917
Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu
175                                180                                185                                190
aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965
Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys
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          195          200          205
tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013
Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu
          210          215          220
tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061
Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly
          225          230          235
ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109
Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile
          240          245          250
gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt 1159
Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
          255          260
aacattaatt ctactaaata ttttatatga aatggtttcac tatgattttc tattttttctt 1219
ctaaaatgct tttaattaat atgttcatta aattttctat gottattgta cttgtttacca 1279
aaaaaaaaaa aaaaaa 1294

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<210> 48  
 <211> 291  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..28

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<400> 48
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          -10          -5          1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5          10          15          20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
          25          30          35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
          40          45          50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
          55          60          65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
70          75          80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
85          90          95          100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
          105          110          115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
          120          125          130
Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
          135          140          145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
          150          155          160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165          170          175          180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
          185          190          195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
          200          205          210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
          215          220          225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
          230          235          240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245          250          255          260

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Lys Asn Met

<210> 49  
 <211> 1194  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..47

<220>  
 <221> CDS  
 <222> 48..1100

<220>  
 <221> 3'UTR  
 <222> 1101..1194

<220>  
 <221> polyA\_signal  
 <222> 1159..1164

<220>  
 <221> polyA\_site  
 <222> 1179..1194

<400> 49  
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 Met Pro Ser  
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104  
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
 -20 -15 -10 -5  
 cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152  
 Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu  
 1 5 10  
 ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200  
 Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu  
 15 20 25  
 ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248  
 Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu  
 30 35 40  
 cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296  
 Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu  
 45 50 55 60  
 gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344  
 Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala  
 65 70 75  
 ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac 392  
 Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn  
 80 85 90  
 gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag 440  
 Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys  
 95 100 105  
 gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488  
 Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe  
 110 115 120  
 aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag 536  
 Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu  
 125 130 135 140  
 gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag 584  
 Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys  
 145 150 155

cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg 632  
 Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp  
 160 165 170  
 gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg 680  
 Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu  
 175 180 185  
 cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat 728  
 Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp  
 190 195 200  
 atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776  
 Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu  
 205 210 215 220  
 cat tta ccc aaa ctg tcc att act gga acc tat gat ctg aag agc gtc 824  
 His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val  
 225 230 235  
 ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg gct gac ctc 872  
 Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu  
 240 245 250  
 tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag gcc gtg cat 920  
 Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His  
 255 260 265  
 aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct gct ggg gcc 968  
 Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala  
 270 275 280  
 atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag gtc aag ttc 1016  
 Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe  
 285 290 295 300  
 aac aaa ccc ttt gtc ttc tta atg att gac caa aat acc aag tct ccc 1064  
 Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr Lys Ser Pro  
 305 310 315  
 ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa taactgcctc 1110  
 Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys  
 320 325  
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 ttgagctgaa aaaaaaaaaa aaaa 1194

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 <211> 351  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..24

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 Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln  
 10 15 20  
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp  
 25 30 35 40  
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly  
 45 50 55  
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His  
 60 65 70  
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys  
 75 80 85  
 Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp  
 90 95 100  
 Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr



105					110					115				120
Ile	Phe	Phe	Lys	Gly	Lys	Trp	Glu	Arg	Pro	Phe	Glu	Val	Lys	Asp
				125					130					135
Glu	Glu	Glu	Asp	Phe	His	Val	Asp	Gln	Val	Thr	Thr	Val	Lys	Val
			140					145					150	
Met	Met	Lys	Arg	Leu	Gly	Met	Phe	Asn	Ile	Gln	His	Cys	Lys	Leu
		155					160					165		
Ser	Ser	Trp	Val	Leu	Leu	Met	Lys	Tyr	Leu	Gly	Asn	Ala	Thr	Ala
		170				175					180			
Phe	Phe	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Gln	His	Leu	Glu	Asn	Glu
185				190					195					200
Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg
			205						210				215	
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp
		220						225					230	
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn
		235					240					245		
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser
	250					255				260				
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu
265					270				275					280
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro
			285					290					295	
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Asp	Gln	Asn
		300					305					310		
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys
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 <212> DNA  
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 <222> 1..289

<220>  
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 <222> 290..1162

<220>  
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 <222> 1163..1317

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 <222> 1269..1274

<220>  
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 <222> 1302..1317

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 gattgcgttt ctttcagtta ctcttcaatc gccagtttct tgatctgctt ctaaaagaag 180  
 aagtagagaa gataaatcct gtcttcaata cctggaagga aaaacaaaat aacctcaact 240  
 ccggttttgaa aaaaacattc caagaacttt catcagagat tttacttag atg att tac 298  
 Met Ile Tyr  
 -25  
 aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ctt 346  
 Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu

				-20					-15					-10			
aat	ctt	gcc	cct	gcc	cct	ctt	aat	gct	gat	tct	gag	gaa	gat	gaa	gaa		394
Asn	Leu	Ala	Pro	Ala	Pro	Leu	Asn	Ala	Asp	Ser	Glu	Glu	Asp	Glu	Glu		
			-5					1				5					
cac	aca	att	atc	aca	gat	acg	gag	ttg	cca	cca	ctg	aaa	ctt	atg	cat		442
His	Thr	Ile	Ile	Thr	Asp	Thr	Glu	Leu	Pro	Pro	Leu	Lys	Leu	Met	His		
	10					15					20						
tca	ttt	tgt	gca	ttc	aag	tcg	gat	gat	ggc	cca	tgt	aaa	gca	atc	atg		490
Ser	Phe	Cys	Ala	Phe	Lys	Ser	Asp	Asp	Gly	Pro	Cys	Lys	Ala	Ile	Met		
	25				30				35				40				
aaa	aga	ttt	ttc	ttc	aat	att	ttc	act	cga	cag	tgc	gaa	gaa	ttt	ata		538
Lys	Arg	Phe	Phe	Phe	Asn	Ile	Phe	Thr	Arg	Gln	Cys	Glu	Glu	Phe	Ile		
			45					50					55				
tat	ggg	gga	tgt	gaa	gga	aat	cag	aat	cga	ttt	gaa	agt	ctg	gaa	gag		586
Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser	Leu	Glu	Glu		
			60					65					70				
tgc	aaa	aaa	atg	tgt	aca	aga	gaa	aag	cca	gat	ttc	tgc	ttt	ttg	gaa		634
Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys	Phe	Leu	Glu		
	75						80					85					
gaa	gat	cct	gga	ata	tgt	cga	ggg	tat	att	acc	agg	tat	ttt	tat	aac		682
Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr	Phe	Tyr	Asn		
	90					95					100						
aat	cag	aca	aaa	cag	tgt	gaa	cgt	ttc	aag	tat	ggg	gga	tgc	ctg	ggc		730
Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly	Cys	Leu	Gly		
	105				110				115					120			
aat	atg	aac	aat	ttt	gag	aca	ctg	gaa	gaa	tgc	aag	aac	att	tgt	gaa		778
Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu		
				125				130					135				
gat	ggg	ccg	aat	ggg	ttc	cag	gtg	gat	aat	tat	gga	acc	cag	ctc	aat		826
Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn		
			140					145					150				
gct	gtg	aat	aac	tcc	ctg	act	ccg	caa	tca	acc	aag	ggt	ccc	agc	ctt		874
Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu		
		155					160					165					
ttt	gaa	ttt	cac	ggg	ccc	tca	tgg	tgt	ctc	act	cca	gca	gac	aga	gga		922
Phe	Glu	Phe	His	Gly	Pro	Ser	Trp	Cys	Leu	Thr	Pro	Ala	Asp	Arg	Gly		
	170				175						180						
ttg	tgt	cgt	gcc	aat	gag	aac	aga	ttc	tac	tac	aat	tca	gtc	att	ggg		970
Leu	Cys	Arg	Ala	Asn	Glu	Asn	Arg	Phe	Tyr	Tyr	Asn	Ser	Val	Ile	Gly		
	185				190				195					200			
aaa	tgc	cgc	cca	ttt	aag	tac	agt	gga	tgt	ggg	gga	aat	gaa	aac	aat		1018
Lys	Cys	Arg	Pro	Phe	Lys	Tyr	Ser	Gly	Cys	Gly	Gly	Asn	Glu	Asn	Asn		
				205				210					215				
ttt	act	tcc	aaa	caa	gaa	tgt	ctg	agg	gca	tgt	aaa	aaa	ggg	ttc	atc		1066
Phe	Thr	Ser	Lys	Gln	Glu	Cys	Leu	Arg	Ala	Cys	Lys	Lys	Gly	Phe	Ile		
			220					225					230				
caa	aga	ata	tca	aaa	gga	ggc	cta	att	aaa	acc	aaa	aga	aaa	aga	aag		1114
Gln	Arg	Ile	Ser	Lys	Gly	Gly	Leu	Ile	Lys	Thr	Lys	Arg	Lys	Arg	Lys		
	235						240					245					
aag	cag	aga	gtg	aaa	ata	gca	tat	gaa	gaa	att	ttt	ggt	aaa	aat	atg		1162
Lys	Gln	Arg	Val	Lys	Ile	Ala	Tyr	Glu	Glu	Ile	Phe	Val	Lys	Asn	Met		
	250				255						260						
tgaatttggt	atagcaatgt	aacattaatt	ctactaaata	ttttatatga	aatgttttcac												1222
tatgattttc	tattttttctt	ctaaaatgct	tttaattaat	atgttcatta	aattttctat												1282
gcttattgta	cttggttatca	aaaaaaaaaa	aaaaa														1317

<210> 52  
 <211> 291  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

<222> 1..28

<400> 52

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Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
      -25                      -20                      -15
Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
      -10                      -5                      1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5                      10                      15                      20
Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
      25                      30                      35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
      40                      45                      50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
      55                      60                      65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
      70                      75                      80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
85                      90                      95                      100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
      105                      110                      115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
      120                      125                      130
Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
      135                      140                      145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
      150                      155                      160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165                      170                      175                      180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
      185                      190                      195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
      200                      205                      210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
      215                      220                      225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
      230                      235                      240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245                      250                      255                      260
Lys Asn Met
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<210> 53

<211> 1907

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..1043

<220>

<221> CDS

<222> 1044..1664

<220>

<221> 3'UTR

<222> 1665..1907

<220>

<221> polyA\_signal

<222> 1869..1874

<220>

<221> polyA\_site  
 <222> 1892..1907

<400> 53

caaaaaaatt	ctaggtcatg	atccccataa	atgaagagtg	atcagtccaa	tcccagggaa	60
cctggacatt	ttgggtattg	tttcagtggg	acatgccttt	cataagttcc	atcttcttgg	120
gtatctctta	ggaagcaagc	ataggaaaca	ggcccatccg	tctgcctgtt	ttgcttcctc	180
atctcacttc	tacacgaggg	tgctgtgtct	caattgctgt	tttcccctaa	agagactctt	240
ttccataagt	ttgtgaaatg	ccatcgacaa	acctgatcgc	attgcatttc	actctgctgt	300
tgagtcgatt	tttctttatt	ttatcattta	gtaactcctt	gctctacaga	gctttcacct	360
tccacatatt	tcagattcat	tctttcctaa	actatgtggg	gggtctacgtc	ctcactgact	420
tatcaacatg	ctaccatcat	gcacttccta	tctctattcc	tcttctttaa	atcttggttcc	480
aaatggctca	caccattatt	ctgagctatt	acctgcctac	gcagtcctag	aaagtaagtg	540
attcaggaaa	cattccccaa	aagtaaaagt	tctcaggtaa	gatcagaaga	ctcccatgag	600
tcactgctgc	tcaggatcac	atctggctcc	ttgaagagtg	attcatcaga	ccttacatag	660
atcttgtcat	aaaaatgaaa	gaggcctcgg	gggaaggctc	tgggctgggtg	gcttctgttg	720
gagtcctggg	ctgtgggggtg	aaagccgtgg	ctgtagagct	tcatgcggag	ttacttagct	780
ttgctctcct	gtggacaggc	catgcctgtg	cctcccccaa	gcacgcggaa	aattggcata	840
gatgggccct	tctcaaaaat	cccactcctg	gagcactggc	caaaattact	accatcctga	900
tgctgggctt	gcagtccttt	cctttgggaa	tatgaacatg	gtcaaaatta	agtgaacgtg	960
tctttctggc	tttctgtaca	atggagcaga	acaaagtatc	aatttaacta	aaatttgaac	1020
taaatcctct	ttccaggttt	gga atg cac ttc tgt gga ggc acc ttg ata tcc				1073
		Met His Phe Cys Gly Gly Thr Leu Ile Ser				
		1 5 10				
cca gag tgg gtg ttg act gct gcc cac tgc ttg gag aag tcc cca agg						1121
Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser Pro Arg						
	15 20 25					
cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg aat ctc						1169
Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val Asn Leu						
	30 35 40					
gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg ttc ttg gag ccc						1217
Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu Glu Pro						
	45 50 55					
aca cga aaa gat att gcc ttg cta aag cta agc agt cct gcc gtc atc						1265
Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val Ile						
	60 65 70					
act gac aaa gta atc cca gct tgt ctg cca tcc cca aat tat gtg gtc						1313
Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr Val Val						
	75 80 85 90					
gct gac cgg acc gaa tgt ttc atc act ggc tgg gga gaa acc caa ggt						1361
Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly						
	95 100 105					
act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc cct gtg att gag						1409
Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val Ile Glu						
	110 115 120					
aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga aga gtc caa tcc						1457
Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser						
	125 130 135					
acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt tgc cag						1505
Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser Cys Gln						
	140 145 150					
ggg gac agt gga ggt cct ctg gtt tgc ttc gag aag gac aaa tac att						1553
Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile						
	155 160 165 170					
tta caa gga gtc act tct tgg ggt ctt ggc tgt gca cgc ccc aat aag						1601
Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys						
	175 180 185					
cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act tgg att gag gga						1649
Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu Gly						
	190 195 200					
gtg atg aga aat aat taattggacg ggagacagag tgacgcactg actcacctag						1704
Val Met Arg Asn Asn						
	205					

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aggctggaac gtgggtaggg atttagcatg ctggaaataa ctggcagtaa tcaaacgaag 1764
acactgtccc cagctaccag ctatgccaaa cctcggcatt ttttgtgtta ttttctgact 1824
gctggattct gtagtaaggt gacatagcta tgacatttgt taaaaataaa ctctgtactt 1884
aactttgaaa aaaaaaaaaa aaa
1907

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<210> 54
<211> 207
<212> PRT
<213> Homo sapiens

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<400> 54
Met His Phe Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr
1      5      10      15
Ala Ala His Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val
20     25     30
Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
35     40     45
Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
50     55     60
Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
65     70     75     80
Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
85     90     95
Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
100    105    110
Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg
115    120    125
Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
130    135    140
His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
145    150    155    160
Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
165    170    175
Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
180    185    190
Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
195    200    205

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<210> 55
<211> 809
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..25

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<220>
<221> CDS
<222> 26..628

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<220>
<221> 3'UTR
<222> 629..809

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<220>
<221> polyA_signal
<222> 766..771

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<220>
<221> polyA_site
<222> 795..809

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			Met	Leu	Glu	Val	Ser	Asp	Ala	Leu	Gly					
			1				5									
gga	cct	gga	aga	gta	cca	ggg	gcc	aca	gca	ggg	atg	aat	gga	gtg	gac	100
Gly	Pro	Gly	Arg	Val	Pro	Gly	Ala	Thr	Ala	Gly	Met	Asn	Gly	Val	Asp	
10					15					20					25	
acg	tcg	ctt	ctc	tgt	gat	ttg	ttg	cag	gcc	ctg	acc	ttc	ctg	acc	aga	148
Thr	Ser	Leu	Leu	Cys	Asp	Leu	Leu	Gln	Ala	Leu	Thr	Phe	Leu	Thr	Arg	
				30				35						40		
aat	gaa	att	ctg	tgc	atc	cat	gac	acc	ttc	ctg	aag	ctc	tgc	cct	cct	196
Asn	Glu	Ile	Leu	Cys	Ile	His	Asp	Thr	Phe	Leu	Lys	Leu	Cys	Pro	Pro	
			45					50					55			
ggg	aag	tac	tac	aag	gag	gca	acg	ctc	acc	atg	gac	cag	gtc	agc	tcc	244
Gly	Lys	Tyr	Tyr	Lys	Glu	Ala	Thr	Leu	Thr	Met	Asp	Gln	Val	Ser	Ser	
		60					65					70				
ctg	cca	gct	ctg	cgg	gtc	aac	cct	ttc	aga	gac	cgt	atc	tgc	aga	gtg	292
Leu	Pro	Ala	Leu	Arg	Val	Asn	Pro	Phe	Arg	Asp	Arg	Ile	Cys	Arg	Val	
	75					80					85					
ttc	tcc	cac	aaa	ggc	atg	ttc	tcc	ttt	gag	gat	gtg	ctg	ggc	atg	gca	340
Phe	Ser	His	Lys	Gly	Met	Phe	Ser	Phe	Glu	Asp	Val	Leu	Gly	Met	Ala	
90				95						100					105	
tct	gtg	ttc	agc	gag	cag	gcc	tgc	cca	agc	ctg	aag	att	gag	tat	gcc	388
Ser	Val	Phe	Ser	Glu	Gln	Ala	Cys	Pro	Ser	Leu	Lys	Ile	Glu	Tyr	Ala	
				110					115					120		
ttt	cgc	atc	tat	gat	ttt	aat	gag	aat	ggc	ttc	att	gat	gag	gag	gat	436
Phe	Arg	Ile	Tyr	Asp	Phe	Asn	Glu	Asn	Gly	Phe	Ile	Asp	Glu	Glu	Asp	
			125					130					135			
ctg	cag	agg	atc	atc	ctg	cga	ctg	ctg	aac	agt	gat	gac	atg	tct	gag	484
Leu	Gln	Arg	Ile	Ile	Leu	Arg	Leu	Leu	Asn	Ser	Asp	Asp	Met	Ser	Glu	
		140					145					150				
gac	ctc	ctg	atg	gac	ctc	acg	aac	cac	gtc	ctg	agt	gag	tcg	gat	ctg	532
Asp	Leu	Leu	Met	Asp	Leu	Thr	Asn	His	Val	Leu	Ser	Glu	Ser	Asp	Leu	
		155				160					165					
gac	aat	gac	aac	atg	ctg	tcc	ttc	tca	gag	ttt	gaa	cat	gca	atg	gcc	580
Asp	Asn	Asp	Asn	Met	Leu	Ser	Phe	Ser	Glu	Phe	Glu	His	Ala	Met	Ala	
170					175					180					185	
aag	tct	cca	gat	ttc	atg	aac	tcc	ttt	cgg	att	cac	ttc	tgg	gga	tgc	628
Lys	Ser	Pro	Asp	Phe	Met	Asn	Ser	Phe	Arg	Ile	His	Phe	Trp	Gly	Cys	
				190					195					200		
tgatgtagcg	gcaaatacct	gacatggcag	cctcgaggga	gaccacagga	atcgaacccc	688										
ctccagcact	ggagggagct	ggtttgaagt														

<210> 56

<211> 201

<212> PRT

<213> Homo sapiens

<400> 56

Met 1	Leu	Glu	Val	Ser 5	Asp	Ala	Leu	Gly	Gly 10	Pro	Gly	Arg	Val	Pro 15	Gly
Ala	Thr	Ala	Gly 20	Met	Asn	Gly	Val	Asp 25	Thr	Ser	Leu	Leu	Cys 30	Asp	Leu
Leu	Gln	Ala 35	Leu	Thr	Phe	Leu	Thr 40	Arg	Asn	Glu	Ile	Leu 45	Cys	Ile	His
Asp	Thr 50	Phe	Leu	Lys	Leu	Cys 55	Pro	Pro	Gly	Lys	Tyr 60	Tyr	Lys	Glu	Ala
Thr 65	Leu	Thr	Met	Asp	Gln 70	Val	Ser	Ser	Leu 75	Pro	Ala	Leu	Arg	Val	Asn 80
Pro	Phe	Arg	Asp	Arg 85	Ile	Cys	Arg	Val	Phe 90	Ser	His	Lys	Gly 95	Met	Phe

Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala  
 100 105 110  
 Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn  
 115 120 125  
 Glu Asn Gly Phe Ile Asp Glu Glu Asp Leu Gln Arg Ile Ile Leu Arg  
 130 135 140  
 Leu Leu Asn Ser Asp Asp Met Ser Glu Asp Leu Leu Met Asp Leu Thr  
 145 150 155 160  
 Asn His Val Leu Ser Glu Ser Asp Leu Asp Asn Asp Asn Met Leu Ser  
 165 170 175  
 Phe Ser Glu Phe Glu His Ala Met Ala Lys Ser Pro Asp Phe Met Asn  
 180 185 190  
 Ser Phe Arg Ile His Phe Trp Gly Cys  
 195 200

<210> 57  
 <211> 1133  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..475

<220>  
 <221> CDS  
 <222> 476..964

<220>  
 <221> 3'UTR  
 <222> 965..1133

<220>  
 <221> polyA\_signal  
 <222> 1101..1106

<220>  
 <221> polyA\_site  
 <222> 1118..1133

<400> 57  
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 gagccaggag gtggcaggac gagttaggag gctgggttcag tagctcgggc aagagcaggg 120  
 cccccaggga tctgaaggcc tcccaggccc cccaggccca gcgggtccca gaggagagcg 180  
 aggaccccaa ggtaactccg gtgagaaggg cgaccaggga tttcaaggcc agccaggctt 240  
 tccgggcccc ccgggtcccc ctggattccc aggcaaagtt ggatcacctg gcccacctgg 300  
 ccctcaagca gagaagggca gcgaagggat tcgaggccca tcaggcctgc ctggctcccc 360  
 tgggccaccg ggacctcctg ggattcaggg ccccgccggg ctggatgggt tggatgggaa 420  
 ggatggcaag cctggcttga ggggggaccc tggtcctgct ggccccctg gactc atg 478  
 Met  
 1  
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526  
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly  
 5 10 15  
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574  
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg  
 20 25 30  
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622  
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro  
 35 40 45  
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670  
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Gly Gln Pro Gly  
 50 55 60 65

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cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
      70      75      80
gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
      85      90      95
cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
      100      105      110
ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
      115      120      125
cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
      130      135      140      145
atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
      150      155      160
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
Phe Gly
ccaaagctta taggactctg tgacagggttg tgaatgtttt ttttgttggt gttgttggtt 1074
ttaattgctg ttaatatattt ttaaataata aagaaacaaa actaaaaaaaa aaaaaaaaaa 1133

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<210> 58  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

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<400> 58
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1      5      10      15
Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly
      20      25      30
Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
      35      40      45
Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
      50      55      60
Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
65      70      75      80
Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
      85      90      95
Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
      100      105      110
Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
      115      120      125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
      130      135      140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
145      150      155      160
Pro Phe Gly

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<210> 59  
 <211> 838  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..78

<220>  
 <221> CDS  
 <222> 79..642



<220>  
 <221> 3'UTR  
 <222> 643..838

<220>  
 <221> polyA\_signal  
 <222> 799..804

<220>  
 <221> polyA\_site  
 <222> 823..838

<400> 59  
 aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggctc 60  
 cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111  
                   Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met  
                   1                  5                  10  
 aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159  
 Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp  
                   15                  20                  25  
 aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg 207  
 Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu  
                   30                  35                  40  
 gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255  
 Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala  
                   45                  50                  55  
 gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303  
 Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys  
                   60                  65                  70                  75  
 gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351  
 Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp  
                   80                  85                  90  
 gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399  
 Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys  
                   95                  100                  105  
 gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447  
 Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp  
                   110                  115                  120  
 cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495  
 His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His  
                   125                  130                  135  
 gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543  
 Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu  
                   140                  145                  150                  155  
 tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591  
 Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly  
                   160                  165                  170  
 gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639  
 Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser  
                   175                  180                  185  
 aaa tgaagatact gacaccacct ttgcctcccc cgtcaccgcg caccacacct 692  
 Lys  
 gaccctcccc tcagctgtcc tgtgccccgc cctctccccgc acactcagtc cccctgcctg 752  
 gcgttccctgc cgcagctctg acctggtgct gtgcacctgg catcttaata aamcctgctt 812  
 atacttccct aaaaaaaaaa aaaaaa 838

<210> 60  
 <211> 188  
 <212> PRT  
 <213> Homo sapiens

<400> 60

Met	Cys	Phe	Pro	Lys	Val	Leu	Ser	Asp	Asp	Met	Lys	Lys	Leu	Lys	Ala	
1				5					10					15		
Arg	Met	His	Gln	Ala	Ile	Glu	Arg	Phe	Tyr	Asp	Lys	Met	Gln	Asn	Ala	
			20					25					30			
Glu	Ser	Gly	Arg	Gly	Gln	Val	Met	Ser	Ser	Leu	Ala	Glu	Leu	Glu	Asp	
		35					40					45				
Asp	Phe	Lys	Glu	Gly	Tyr	Leu	Glu	Thr	Val	Ala	Ala	Tyr	Tyr	Glu	Glu	
	50					55					60					
Gln	His	Pro	Glu	Leu	Thr	Pro	Leu	Leu	Glu	Lys	Glu	Arg	Asp	Gly	Leu	
65					70					75					80	
Arg	Cys	Arg	Gly	Asn	Arg	Ser	Pro	Val	Pro	Asp	Val	Glu	Asp	Pro	Ala	
				85					90					95		
Thr	Glu	Glu	Pro	Gly	Glu	Ser	Phe	Cys	Asp	Lys	Val	Met	Arg	Trp	Phe	
			100					105						110		
Gln	Ala	Met	Leu	Gln	Arg	Leu	Gln	Thr	Trp	Trp	His	Gly	Val	Leu	Ala	
		115					120					125				
Trp	Val	Lys	Glu	Lys	Val	Val	Ala	Leu	Val	His	Ala	Val	Gln	Ala	Leu	
	130					135					140					
Trp	Lys	Gln	Phe	Gln	Ser	Phe	Cys	Cys	Ser	Leu	Ser	Glu	Leu	Phe	Met	
145					150					155					160	
Ser	Ser	Phe	Gln	Ser	Tyr	Gly	Ala	Pro	Arg	Gly	Asp	Lys	Glu	Glu	Leu	
				165					170						175	
Thr	Pro	Gln	Lys	Cys	Ser	Glu	Pro	Gln	Ser	Ser	Lys					
			180					185								

<210> 61  
 <211> 862  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..158

<220>  
 <221> CDS  
 <222> 159..764

<220>  
 <221> 3'UTR  
 <222> 765..862

<400> 61  
 attttttttt ttggcacgcc tgcagccaag ttggggaggg tttcctggac agaggtcctt 60  
 tggctgctgc cttaagacgt gcagcctggg ccgtggctgt cactgcgttc ggaccagac 120  
 ccgctgcagg cagcagcagc ccccgcgcgc gcagcagc atg gag ctc tgg ggg gcc 176  
 Met Glu Leu Trp Gly Ala  
 -20 -15  
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224  
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu  
 -10 -5 1  
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272  
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val  
 5 10 15  
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320  
 Val Asn Thr Lys Met Phe Glu Leu Lys Ser Arg Leu Asp Thr Leu  
 20 25 30  
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368  
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val  
 35 40 45 50  
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416  
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr  
 55 60 65

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cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464
Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
      70      75      80
ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512
Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
      85      90      95
gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560
Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
      100      105      110
ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608
Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
      115      120      125      130
cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
      135      140      145
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
      150      155      160
aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
      165      170      175
ttc ggg atc gtg tagccggcgg ggcgggggcc gtgggggggcc tggaggaggg 804
Phe Gly Ile Val
      180
caggagccgc gggaggccgg gaggaggggtg gggaccttgc agcccccatc ctctccgt 862

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<210> 62
<211> 202
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..21

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<400> 62
Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu
  -20      -15      -10
Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
  -5      1      5      10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
      15      20      25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
      30      35      40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
      45      50      55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
      60      65      70      75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
      80      85      90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
      95      100      105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
      110      115      120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
      125      130      135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
      140      145      150      155
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
      160      165      170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
      175      180

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<210> 63  
 <211> 618  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..194

<220>  
 <221> CDS  
 <222> 195..587

<220>  
 <221> 3'UTR  
 <222> 588..618

<220>  
 <221> polyA\_signal  
 <222> 578..583

<220>  
 <221> polyA\_site  
 <222> 604..618

<400> 63  
 atttgcttag gtctgatcaa tctgctccac acaatttctc agtgatcctc tgcattctctg 60  
 cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120  
 ttctgttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180  
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230  
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu  
 -20 -15 -10  
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278  
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala  
 -5 1 5  
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326  
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln  
 10 15 20  
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374  
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala  
 25 30 35  
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422  
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr  
 40 45 50 55  
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470  
 Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser  
 60 65 70  
 atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518  
 Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg  
 75 80 85  
 act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566  
 Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met  
 90 95 100  
 tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618  
 Cys Phe Ala Leu Leu Asn Cys  
 105 110

<210> 64  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..22

<400> 64

Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly  
-20 -15 -10  
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln  
-5 1 5 10  
Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu  
15 20 25  
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln  
30 35 40  
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala  
45 50 55  
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile  
60 65 70  
Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg Thr Ala Gly Ala  
75 80 85 90  
Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met Cys Phe Ala Leu  
95 100 105  
Leu Asn Cys

<210> 65

<211> 836

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..176

<220>

<221> CDS

<222> 177..767

<220>

<221> 3'UTR

<222> 768..836

<220>

<221> polyA\_signal

<222> 814..819

<220>

<221> polyA\_site

<222> 822..836

<400> 65

aatctgctcc acgcaatttc tcagtgatcc tctgcatctc tgccatacaag ggcctccctg 60  
acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120  
ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaatata tggaaa atg 179  
Met  
aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227  
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu  
-20 -15 -10 -5  
gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275  
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser  
1 5 10  
gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg 323  
Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu  
15 20 25  
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371  
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser

30	35	40	
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg			419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu			
45	50	55	60
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa			467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys			
65	70	75	
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg			515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met			
80	85	90	
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc			563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu			
95	100	105	
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct			611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro			
110	115	120	
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc			659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu			
125	130	135	140
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc			707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser			
145	150	155	
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt			755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu			
160	165	170	
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaaatatg			807
Phe Ser Pro Ala			
175			
atagtgtata aatgaaaaaa aaaaaaaaaa			836

<210> 66

<211> 197

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..22

<400> 66

Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly	
-20	-15
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln	
-5	1
Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu	10
15	20
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln	25
30	35
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala	40
45	50
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile	55
60	65
Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala	70
75	80
Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys	85
95	100
Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr	105
110	115
Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp	120
125	130
Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn	135
140	145
Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser	150

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155          160          165          170
Leu Phe Ser Pro Ala
          175

<210> 67
<211> 789
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..62

<220>
<221> CDS
<222> 63..572

<220>
<221> 3'UTR
<222> 573..789

<220>
<221> polyA_signal
<222> 750..755

<220>
<221> polyA_site
<222> 774..789

<400> 67
atatgtcatc aggccccccg cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60
ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
20 25 30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp

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160                      165                      170
gaggaggggac gccacgggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652
caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772
gaaaaaaaaa aaaaaaa                                     789

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<210> 68
<211> 170
<212> PRT
<213> Homo sapiens

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<400> 68
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1                      5                      10                      15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
20                      25                      30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35                      40                      45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50                      55                      60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65                      70                      75                      80
Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85                      90                      95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100                     105                     110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115                     120                     125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130                     135                     140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145                     150                     155                     160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165                      170

```

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<210> 69
<211> 2556
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..66

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<220>
<221> CDS
<222> 67..2427

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<220>
<221> 3'UTR
<222> 2428..2556

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<220>
<221> polyA_signal
<222> 2522..2527

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<220>
<221> polyA_site
<222> 2541..2556

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<400> 69
gtccccgcgt ccctggcaat tcccgaacttc ccaacggctt cctgctggca gccccgaagc 60
cgcacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108

```



Met	Phe	Arg	Leu	Trp	Leu	Leu	Leu	Ala	Gly	Leu	Cys	Gly	Leu			
-15					-10					-5						
ctg	gcg	tca	aga	ccc	ggg	ttt	caa	aat	tca	ctt	cta	cag	atc	gta	att	156
Leu	Ala	Ser	Arg	Pro	Gly	Phe	Gln	Asn	Ser	Leu	Leu	Gln	Ile	Val	Ile	
1					5				10					15		
cca	gag	aaa	atc	caa	aca	aat	aca	aat	gac	agt	tca	gaa	ata	gaa	tat	204
Pro	Glu	Lys	Ile	Gln	Thr	Asn	Thr	Asn	Asp	Ser	Ser	Glu	Ile	Glu	Tyr	
				20					25					30		
gaa	caa	ata	tcc	tat	att	att	cca	ata	gat	gag	aaa	ctg	tac	act	gtg	252
Glu	Gln	Ile	Ser	Tyr	Ile	Ile	Pro	Ile	Asp	Glu	Lys	Leu	Tyr	Thr	Val	
			35						40					45		
cac	ctt	aaa	caa	aga	tat	ttt	tta	aca	gat	aat	ttt	atg	atc	tat	ttg	300
His	Leu	Lys	Gln	Arg	Tyr	Phe	Leu	Thr	Asp	Asn	Phe	Met	Ile	Tyr	Leu	
		50					55					60				
tac	aat	caa	gga	tct	atg	aat	act	tat	tct	tca	gat	att	cag	act	caa	348
Tyr	Asn	Gln	Gly	Ser	Met	Asn	Thr	Tyr	Ser	Ser	Asp	Ile	Gln	Thr	Gln	
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tgc	tac	tat	caa	gga	aat	att	gaa	gaa	tat	cca	gat	tcc	atg	gtc	aca	396
Cys	Tyr	Tyr	Gln	Gly	Asn	Ile	Glu	Glu	Tyr	Pro	Asp	Ser	Met	Val	Thr	
80					85					90				95		
ctc	agc	acg	tgc	tct	gga	cta	aga	gga	ata	ctg	caa	ttt	gaa	aat	gtt	444
Leu	Ser	Thr	Cys	Ser	Gly	Leu	Arg	Gly	Ile	Leu	Gln	Phe	Glu	Asn	Val	
				100					105					110		
tct	tat	gga	att	gag	cct	ctg	gaa	tct	gca	gtt	gaa	ttt	cag	cat	gtt	492
Ser	Tyr	Gly	Ile	Glu	Pro	Leu	Glu	Ser	Ala	Val	Glu	Phe	Gln	His	Val	
		115						120					125			
ctt	cac	aaa	tta	aag	aat	gaa	gac	aat	gat	att	gca	att	ttt	att	gac	540
Leu	His	Lys	Leu	Lys	Asn	Glu	Asp	Asn	Asp	Ile	Ala	Ile	Phe	Ile	Asp	
		130					135					140				
aga	agc	ctg	aaa	gaa	caa	cca	atg	gat	gac	aac	att	ttt	ata	agt	gaa	588
Arg	Ser	Leu	Lys	Glu	Gln	Pro	Met	Asp	Asp	Asn	Ile	Phe	Ile	Ser	Glu	
		145				150					155					
aaa	tca	gaa	cca	gct	gtt	cca	gat	tta	ttt	cct	ctt	tat	cta	gaa	atg	636
Lys	Ser	Glu	Pro	Ala	Val	Pro	Asp	Leu	Phe	Pro	Leu	Tyr	Leu	Glu	Met	
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cat	att	gtg	gtg	gac	aaa	act	ttg	tat	gat	tac	tgg	ggc	tct	gat	agc	684
His	Ile	Val	Val	Asp	Lys	Thr	Leu	Tyr	Asp	Tyr	Trp	Gly	Ser	Asp	Ser	
				180					185					190		
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Met	Ile	Val	Thr	Asn	Lys	Val	Ile	Glu	Ile	Val	Gly	Leu	Ala	Asn	Ser	
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Met	Phe	Thr	Gln	Phe	Lys	Val	Thr	Ile	Val	Leu	Ser	Ser	Leu	Glu	Leu	
		210					215					220				
tgg	tca	gat	gaa	aat	aag	att	tct	aca	gtt	ggg	gag	gca	gat	gaa	tta	828
Trp	Ser	Asp	Glu	Asn	Lys	Ile	Ser	Thr	Val	Gly	Glu	Ala	Asp	Glu	Leu	
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ttg	caa	aaa	ttt	tta	gaa	tgg	aaa	caa	tct	tat	ctt	aac	cta	agg	cct	876
Leu	Gln	Lys	Phe	Leu	Glu	Trp	Lys	Gln	Ser	Tyr	Leu	Asn	Leu	Arg	Pro	
240					245					250				255		
cat	gat	att	gca	tat	cta	cta	att	tat	atg	gat	tat	cct	cgt	tat	ttg	924
His	Asp	Ile	Ala	Tyr	Leu	Leu	Ile	Tyr	Met	Asp	Tyr	Pro	Arg	Tyr	Leu	
			260					265					270			
gga	gca	gtg	ttt	cct	gga	aca	atg	tgt	att	act	cgt	tat	tct	gca	gga	972
Gly	Ala	Val	Phe	Pro	Gly	Thr	Met	Cys	Ile	Thr	Arg	Tyr	Ser	Ala	Gly	
		275					280					285				
gtc	gca	ttg	tac	ccc	aag	gag	ata	act	ctg	gag	gca	ttt	gca	gtt	att	1020
Val	Ala	Leu	Tyr	Pro	Lys	Glu	Ile	Thr	Leu	Glu	Ala	Phe	Ala	Val	Ile	
		290					295					300				
gtc	acc	cag	atg	ctg	gca	ctc	agt	ctg	gga	ata	tca	tat	gac	gac	cca	1068
Val	Thr	Gln	Met	Leu	Ala	Leu	Ser	Leu	Gly	Ile	Ser	Tyr	Asp	Asp	Pro	
		305				310					315					
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Lys	Lys	Cys	Gln	Cys	Ser	Glu	Ser	Thr	Cys	Ile	Met	Asn	Pro	Glu	Val	
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gtg	caa	tcc	aat	ggg	gtg	aag	act	ttt	agc	agt	tgc	agt	ttg	agg	agc	1164
Val	Gln	Ser	Asn	Gly	Val	Lys	Thr	Phe	Ser	Ser	Cys	Ser	Leu	Arg	Ser	
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Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	
			355					360					365			
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Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	
		370					375					380				
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Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly	
	385					390					395					
cct	gca	agc	tgt	tgt	gat	ttt	cga	act	tgt	gta	ctg	aaa	gac	gga	gca	1356
Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala	
400					405					410					415	
aaa	tgt	tat	aaa	gga	ctg	tgc	tgc	aaa	gac	tgt	caa	att	tta	caa	tca	1404
Lys	Cys	Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser	
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ggc	gtt	gaa	tgt	agg	ccg	aaa	gca	cat	cct	gaa	tgt	gac	atc	gct	gaa	1452
Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu	
			435					440					445			
aat	tgt	aat	gga	agc	tca	cca	gaa	tgt	ggg	cct	gac	ata	act	tta	atc	1500
Asn	Cys	Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile	
		450					455					460				
aat	gga	ctt	tca	tgc	aaa	aat	aat	aag	ttt	att	tgt	tat	gac	gga	gac	1548
Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp	
	465				470					475						
tgc	cat	gat	ctc	gat	gca	cgt	tgt	gag	agt	gta	ttt	gga	aaa	ggg	tca	1596
Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser	
480					485					490				495		
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Arg	Asn	Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp	
			500							505				510		
aga	ttt	ggg	aac	tgt	ggg	agg	gat	aga	aat	aac	aaa	tat	gtg	ttc	tgt	1692
Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys	
			515					520					525			
gga	tgg	agg	aat	ctt	ata	tgt	gga	aga	tta	gtt	tgt	acc	tac	cct	act	1740
Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr	
		530					535					540				
cga	aag	cct	ttc	cat	caa	gaa	aat	ggg	gat	gtg	att	tat	gct	ttc	gta	1788
Arg	Lys	Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val	
	545				550						555					
cga	gat	tct	gta	tgc	ata	acc	gta	gac	tac	aaa	ttg	cct	cga	aca	gtt	1836
Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val	
560					565					570				575		
cca	gat	cca	ctg	gct	gtc	aaa	aat	ggc	tct	cag	tgt	gat	att	ggg	agg	1884
Pro	Asp	Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg	
			580						585					590		
gtt	tgt	gta	aat	cgt	gaa	tgt	gta	gaa	tca	agg	ata	att	aag	gct	tca	1932
Val	Cys	Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser	
			595					600					605			
gca	cat	gtt	tgt	tca	caa	cag	tgt	tct	gga	cat	gga	gtg	tgt	gat	tcc	1980
Ala	His	Val	Cys	Ser	Gln	Gln	Cys	Ser	Gly	His	Gly	Val	Cys	Asp	Ser	
		610					615					620				
aga	aac	aag	tgc	cat	tgt	tgc	cca	ggc	tat	aag	cct	cca	aac	tgc	caa	2028
Arg	Asn	Lys	Cys	His	Cys	Ser	Pro	Gly	Tyr	Lys	Pro	Pro	Asn	Cys	Gln	
		625				630					635					
ata	cgt	tcc	aaa	gga	ttt	tcc	ata	ttt	cct	gag	gaa	gat	atg	ggg	tca	2076
Ile	Arg	Ser	Lys	Gly	Phe	Ser	Ile	Phe	Pro	Glu	Glu	Asp	Met	Gly	Ser	
640					645					650					655	
atc	atg	gaa	aga	gca	tct	ggg	aag	act	gaa	aac	acc	tgg	ctt	cta	ggg	2124

Ile Met Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly	
660	665
670	675
ttc ctc att gct ctt cct att ctc att gta aca acc gca ata gtt ttg	2172
Phe Leu Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu	
675	680
685	690
gca agg aaa cag ttg aaa aac tgg ttc gcc aag gaa gag gaa ttc cca	2220
Ala Arg Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro	
690	695
700	705
agt agc gaa tct aaa tcg gaa ggt agc aca cag aca tat gcc agc caa	2268
Ser Ser Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln	
705	710
715	720
tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca	2316
Ser Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser	
720	725
730	735
gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt	2364
Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser	
740	745
750	755
gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca	2412
Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr	
755	760
765	770
caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc	2467
Gln Ser Ser Ser Asn	
770	
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ttgagtgtgg accaaaaaaaaa aaaaaaaaaat	2556

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<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..16

<400> 70

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-5	
Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu	
1	5
10	15
Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln	
20	25
30	35
Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu	
35	40
45	50
Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn	
50	55
60	65
Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr	
65	70
75	80
Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser	
85	90
95	100
Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr	
100	105
110	115
Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His	
115	120
125	130
Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser	
130	135
140	145
Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser	
145	150
155	160
Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile	
165	170
175	180
Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile	
180	185
190	
Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe	



Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser  
 705 710 715 720  
 Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser Glu Ser  
 725 730 735  
 Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu  
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 Ser Ser Asn  
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 <212> DNA  
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 cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97  
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro  
 1 5 10  
 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145  
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu  
 15 20 25 30  
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193  
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile  
 35 40 45  
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241  
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val  
 50 55 60  
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289  
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu  
 65 70 75  
 gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337  
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu  
 80 85 90



Leu	Leu	Asp	Gly	Met	Leu	Asp	Gly	Gln	Val	Asn	Ser	Gly	Ile	Ala	Ala		
			35					40					45				
Thr	Pro	Ala	Ser	Ala	Ala	Ala	Ala	Thr	Leu	Asp	Val	Ala	Val	Arg	Arg		
		50					55					60					
Gly	Leu	Ser	His	Ala	Ala	Gln	Arg	Leu	Leu	Cys	Val	Ala	Leu	Gly	Gln		
	65					70				75							
Leu	Asp	Arg	Pro	Pro	Asp	Leu	Ala	His	Asp	Gly	Arg	Ser	Leu	Trp	Leu		
80					85					90					95		
Asn	Ile	Arg	Gly	Lys	Glu	Ala	Ala	Ala	Leu	Ser	Met	Phe	His	Val	Ser		
				100						105					110		
Thr	Pro	Leu	Pro	Val	Met	Thr	Gly	Gly	Phe	Leu	Ser	Cys	Ile	Leu	Gly		
			115					120							125		
Leu	Val	Leu	Pro	Leu	Ala	Tyr	Gly	Phe	Gln	Pro	Asp	Leu	Val	Leu	Val		
	130						135					140					
Ala	Leu	Gly	Pro	Gly	His	Gly	Leu	Gln	Gly	Pro	His	Xaa	Ala	Leu	Leu		
	145					150					155						
Ala	Ala	Met	Leu	Arg	Gly	Leu	Ala	Gly	Gly	Arg	Val	Leu	Ala	Leu	Leu		
160					165					170					175		
Glu	Glu	Asn	Ser	Thr	Pro	Gln	Leu	Ala	Gly	Ile	Leu	Ala	Arg	Val	Leu		
				180						185					190		
Asn	Gly	Glu	Ala	Pro	Pro	Ser	Leu	Gly	Pro	Ser	Ser	Val	Ala	Ser	Pro		
		195						200						205			
Glu	Asp	Val	Gln	Ala	Leu	Met	Tyr	Leu	Arg	Gly	Gln	Leu	Glu	Pro	Gln		
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<220>  
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<400> 73																	
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	Met	Ala	Val	Leu	Leu	Leu	Leu	Arg	Ala	Leu	Arg	Arg	Gly				
	-15					-10				-5							
cca ggc	cgc	ggg	cct	cgc	ccg	ctg	tgg	ggc	cca	ggc	cgc	gcc	tgg	agt		98	
Pro Gly	Pro Gly	Pro Arg	Pro Leu	Trp	Gly	Pro Gly	Pro Ala	Trp	Ser								
1		5			10		15										
cca ggg	ttc	ccc	gcc	agg	ccc	ggg	agg	ggg	cgc	ccg	tac	atg	gcc	agc		146	
Pro Gly	Phe	Pro Ala	Arg	Pro Gly	Arg	Gly	Arg	Pro Tyr	Met	Ala	Ser						
		20			25		30										
agg cct	ccg	ggg	gac	ctc	gcc	gag	gct	gga	ggc	cga	gct	ctg	cag	agc		194	
Arg Pro	Pro Gly	Asp Leu	Ala Glu	Ala Gly	Gly Arg	Ala Leu	Gln Ser										
	35				40		45										
tta caa	ttg	aga	ctg	cta	acc	cct	acc	ttt	gaa	ggg	atc	aac	gga	ttg		242	
Leu Gln	Leu Arg	Leu Leu	Thr	Pro Thr	Phe Glu	Gly Ile	Asn Gly	Leu									

50	55	60	
ttg ttg aaa caa cat tta gtt	cag aat cca gtc	aga ctc tgg caa ctt	290
Leu Leu Lys Gln His Leu Val	Gln Asn Pro Val Arg Leu Trp	Gln Leu	
65	70	75	
tta ggt ggt act ttc tat ttt	aac acc tca agg ttg aag	cag aag aat	338
Leu Gly Gly Thr Phe Tyr Phe	Asn Thr Ser Arg Leu Lys	Gln Lys Asn	
80	85	90	95
aag gag aag gat aag tgc aag	ggg aag gcg cct gaa gag	gac gaa ggt	386
Lys Glu Lys Asp Lys Ser Lys	Gly Lys Ala Pro Glu Glu	Asp Glu Gly	
100	105	110	
ata ttc atc tgatgttctt	cagtcagtag ctgcctctgg	atgtctttac	435
Ile Phe Ile			
rtttctgttt wccttttagc	aaggtgaaac cagtctggam	aatggggaga tggggccgggt	495
gcagtggctc acacttgtaa	tcgaaacgct ttgggaggcc	caggtggaag gatcacttga	555
ggcctatacc acatagctag	accctgtctc actgcaaatt	aaaaggctgg gcgtggtggc	615
tcacacctgt aatcccagca	ctttgggagg ctgaggcagg	cggatcacct gcaccctggc	675
caacatggtg aaaccccgtc	tttactaaaa atagaaaatt	agccgggcgt gatggcacac	735
gcctgtaatc ccagctactc	gggaggctga ggcaggagaa	ttgcttgaac ctgggagggtg	795
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tccatcccaa aaaaaaaaaa	aaaaa		879

<210> 74  
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 <222> 1..16

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Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro	
20 25 30	
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln	
35 40 45	
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu	
50 55 60	
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly	
65 70 75 80	
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu	
85 90 95	
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe	
100 105 110	
Ile	

<210> 75  
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 <212> DNA  
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 <222> 1..87

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<221> 3'UTR
<222> 1270..1634

<220>
<221> polyA_signal
<222> 1594..1599

<220>
<221> polyA_site
<222> 1619..1634

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Met Met Gly Val Phe Val Val Ala Ala
1 5
aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162
Lys Arg Thr Pro Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr
10 15 20 25
gct act gac ttg tct gaa ttt gct gcc aag gct gcc ttg tct gct ggc 210
Ala Thr Asp Leu Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly
30 35 40
aaa gtc tca cct gaa aca gtt gac agt gtg att atg ggc aat gtc ctg 258
Lys Val Ser Pro Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu
45 50 55
cag agt tct tca gat gct ata tat ttg gca agg cat gtt ggt ttg cgt 306
Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg His Val Gly Leu Arg
60 65 70
gtg gga atc cca aag gag acc cca gct ctc acg att aat agg ctc tgt 354
Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr Ile Asn Arg Leu Cys
75 80 85
ggt tct ggt ttt cag tcc att gtg aat gga tgt cag gaa att tgt gtt 402
Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys Gln Glu Ile Cys Val
90 95 100 105
aaa gaa gct gaa gtt gtt tta tgt gga gga acc gaa agc atg agc caa 450
Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr Glu Ser Met Ser Gln
110 115 120
gct ccc tac tgt gtc aga aat gtg cgt ttt gga acc aag ctt gga tca 498
Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly Thr Lys Leu Gly Ser
125 130 135
gat atc aag ctg gaa gat tct tta tgg gta tca tta aca gat cag cat 546
Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser Leu Thr Asp Gln His
140 145 150
gtc cag ctc ccc atg gca atg act gca gag aat ctt gct gta aaa cac 594
Val Gln Leu Pro Met Ala Met Thr Ala Glu Asn Leu Ala Val Lys His
155 160 165
aaa ata agc aga gaa gaa tgt gac aaa tat gcc ctg cag tca cag cag 642
Lys Ile Ser Arg Glu Glu Cys Asp Lys Tyr Ala Leu Gln Ser Gln Gln
170 175 180 185
aga tgg aaa gct gct aat gat gct ggc tac ttt aat gat gaa atg gca 690
Arg Trp Lys Ala Ala Asn Asp Ala Gly Tyr Phe Asn Asp Glu Met Ala
190 195 200
cca att gaa gtg aag aca aag aaa gga aaa cag aca atg cag gta gac 738
Pro Ile Glu Val Lys Thr Lys Lys Gly Lys Gln Thr Met Gln Val Asp
205 210 215
gag cat gct cgg ccc caa acc acc ctg gaa cag tta cag aaa ctt cct 786
Glu His Ala Arg Pro Gln Thr Thr Leu Glu Gln Leu Gln Lys Leu Pro
220 225 230
cca gta ttc aag aaa gat gga act gtt act gca ggg aat gca tcg ggt 834
Pro Val Phe Lys Lys Asp Gly Thr Val Thr Ala Gly Asn Ala Ser Gly
235 240 245
gta gct gat ggt gct gga gct gtt atc ata gct agt gaa gat gct gtt 882
Val Ala Asp Gly Ala Gly Ala Val Ile Ile Ala Ser Glu Asp Ala Val

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250	255	260	265	
aag aaa cat aac ttc	aca cca ctg gca	aga att gtg ggc tac ttt	gta	930
Lys Lys His Asn Phe	Thr Pro Leu Ala Arg	Ile Val Gly Tyr Phe	Val	
	270	275	280	
tct gga tgt gat ccc	tct atc atg ggt	att ggt cct gtc cct	gct atc	978
Ser Gly Cys Asp Pro	Ser Ile Met Gly	Ile Gly Pro Val Pro	Ala Ile	
	285	290	295	
agt ggg gca ctg aag	aaa gca gga ctg	agt ctt aag gac atg	gat ttg	1026
Ser Gly Ala Leu Lys	Lys Ala Gly Leu	Ser Leu Lys Asp	Met Asp Leu	
	300	305	310	
gta gag gtg aat gaa	gct ttt gct ccc	cag tac ttg gct	gtt gag agg	1074
Val Glu Val Asn Glu	Ala Phe Ala Pro	Gln Tyr Leu Ala	Val Glu Arg	
	315	320	325	
agt ttg gat ctt gac	ata agt aaa acc	aat gtg aat gga	gga gcc att	1122
Ser Leu Asp Leu Asp	Ile Ser Lys Thr	Asn Val Asn Gly	Gly Ala Ile	
	330	335	340	345
gct ttg ggt cac cca	ctg gga gga tct	gga tca aga att	act gca cac	1170
Ala Leu Gly His Pro	Leu Gly Gly Ser	Gly Ser Arg Ile	Thr Ala His	
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ctg gtt cac gaa tta	agg cgt cga ggt	gga aaa tat gcc	gtt gga tca	1218
Leu Val His Glu Leu	Arg Arg Arg Gly	Gly Lys Tyr Ala	Val Gly Ser	
	365	370	375	
gct tgc att gga ggt	ggc caa ggt att	gct gtc atc att	cag agc aca	1266
Ala Cys Ile Gly Gly	Gly Gln Gly Ile	Ala Val Ile Ile	Gln Ser Thr	
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gcc tgaagagacc agt	gagctca ctgtgaccca	tccttactct acttggccag		1319
Ala				
gccacagtaa aacaagt	gac cttcagagca	gctgccacaa ctggccatgc	cctgccattg	1379
aaacagtgat taagt	ttgat caagccatgg	tgacacaaaa atgcattgat	catgaatagg	1439
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gctaaaactc aactat	agaa gacattaaaa	gaaatcgtat tcttgccaag	taaccaccac	1559
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<210> 76  
 <211> 394  
 <212> PRT  
 <213> Homo sapiens

<400> 76  
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 35 40 45  
 Asp Ser Val Ile Met Gly Asn Val Leu Gln Ser Ser Asp Ala Ile  
 50 55 60  
 Tyr Leu Ala Arg His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr  
 65 70 75 80  
 Pro Ala Leu Thr Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile  
 85 90 95  
 Val Asn Gly Cys Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu  
 100 105 110  
 Cys Gly Gly Thr Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn  
 115 120 125  
 Val Arg Phe Gly Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser  
 130 135 140  
 Leu Trp Val Ser Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met  
 145 150 155 160  
 Thr Ala Glu Asn Leu Ala Val Lys His Lys Ile Ser Arg Glu Glu Cys  
 165 170 175  
 Asp Lys Tyr Ala Leu Gln Ser Gln Gln Arg Trp Lys Ala Ala Asn Asp





<221> SIGNAL

<222> 1..21

<400> 78

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His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
  -5          1          5          10
Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
      15          20          25
Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
      30          35          40
Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
      45          50          55
Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
      60          65          70          75
Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser
      80          85          90
Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
      95          100          105
Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
      110          115          120
Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
      125          130          135
Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu Asn Met
      140          145          150          155
Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
      160          165          170
Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
      175          180          185
Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
      190          195          200
Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp
      205          210          215
Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
      220          225          230          235
Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
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<210> 79

<211> 1466

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..343

<220>

<221> CDS

<222> 344..1144

<220>

<221> 3'UTR

<222> 1145..1466

<400> 79

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gggccggagg agctgctttc tgaatccaag ttcgtgggct ctctcagaag tcctcaggac 180
ggagcagagg tggccggcgg gcccggtga ctgcgcctyt gctttctttc cataaccttt 240
tctttcggac tcgaatcacg gctgctgcga agggtctagt tccggacact aggggtgccc 300
aacgcgctga tgccccgagt gctcgcaggg cttcccgccta acc atg ctg ccg ccg 355
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ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg 403  
 Pro Arg Pro Ala Ala -20 Leu Ala Leu Pro Val Leu Leu Leu Leu Leu  
 -25 -15 -10  
 gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca tcc cca ggc cca 451  
 Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro  
 -5 1 5  
 gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg gag ggc gag ggc 499  
 Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly  
 10 15 20  
 tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg cgg ggc tgc ctg 547  
 Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro Arg Gly Cys Leu  
 25 30 35  
 gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg gaa tgc gcc aac 595  
 Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp Glu Cys Ala Asn  
 40 45 50 55  
 ctc gag ggc cag ctc tgc gac ctg gac ccc agt gct cac ttc tac ggg 643  
 Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala His Phe Tyr Gly  
 60 65 70  
 cac tgc ggc gag cag ctt gag tgc cgg ctg gac aca ggc ggc gag ctg 691  
 His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr Gly Gly Asp Leu  
 75 80 85  
 agc cgc gga gag gtg ccg gaa cct ctg tgt gcc tgt cgt tgc cag agt 739  
 Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys Arg Ser Gln Ser  
 90 95 100  
 ccg ctc tgc ggg tcc gac ggt cac acc tac tcc cag atc tgc cgc ctg 787  
 Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln Ile Cys Arg Leu  
 105 110 115  
 cag gag gcg gcc cgc gct cgg ccc gat gcc aac ctc act gtg gca cac 835  
 Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu Thr Val Ala His  
 120 125 130 135  
 ccg ggg ccc tgc gaa tcg ggg ccc cag atc gtg tca cat cca tat gac 883  
 Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser His Pro Tyr Asp  
 140 145 150  
 act tgg aat gtg aca ggg cag gat gtg atc ttt ggc tgt gaa gtg ttt 931  
 Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly Cys Glu Val Phe  
 155 160 165  
 gcc tac ccc atg gcc tcc atc gag tgg agg aag gat ggc ttg gac atc 979  
 Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu Asp Ile  
 170 175 180  
 cag ctg cca ggg gat gac ccc cac atc tct gtg cag ttt agg ggt gga 1027  
 Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg Gly Gly  
 185 190 195  
 ccc cag agg ttt gag gtg act ggc tgg ctg cag atc cag gct gtg cgt 1075  
 Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala Val Arg  
 200 205 210 215  
 ccc agt gat gag ggc act tac cgc tgc ctt ggc cca atg ccc tgg gtc 1123  
 Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro Met Pro Trp Val  
 220 225 230  
 aag tgg agg ccc ctg cta gct tgacagtgc cacacctgac cagctgaact 1174  
 Lys Trp Arg Pro Leu Leu Ala  
 235  
 ctacagggcat cccccagctg cgatcactaa acctgggttcc tgaggaggag gctgagagtg 1234  
 aagagaatga cgattactac taggtccaga gctctggccc atgggggtgg gtgagcggct 1294  
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<210> 80

<211> 267

<212> PRT

<213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..30

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 -10 -5 1  
 Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala  
 5 10 15  
 Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro  
 20 25 30  
 Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp  
 35 40 45 50  
 Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala  
 55 60 65  
 His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr  
 70 75 80  
 Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys  
 85 90 95  
 Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln  
 100 105 110  
 Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu  
 115 120 125 130  
 Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser  
 135 140 145  
 His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly  
 150 155 160  
 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp  
 165 170 175  
 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln  
 180 185 190  
 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile  
 195 200 205 210  
 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro  
 215 220 225  
 Met Pro Trp Val Lys Trp Arg Pro Leu Leu Ala  
 230 235

<210> 81  
 <211> 1406  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..26

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 <222> 27..689

<220>  
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 <222> 690..1406

<220>  
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 <222> 1302..1307

<220>  
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<222> 1325..1406

<400> 81

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GlyLeuArgAlaLeuCysArgValLeuLeuPheLeuSerGlnPheCys
-20-15-10
attctgtcggcgggtgaaagtactgaaatccacttatgtgatgaag149
IleLeuSerGlyGlyGluSerThrGluIleProProTyrValMetLys
-51510
tgtccgagcaaatgggttgttgtagcaggcttcctgcaagctgtatagac197
CysProSerAsnGlyLeuCysSerArgLeuProAlaAspCysIleAsp
152025
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CysThrThrAsnPheSerCysThrTyrGlyLysProValThrPheAsp
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CysAlaValLysProSerValThrCysValAspGlnAspPheLysSer
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ProGluThrAspTyrGluCysThrAsnSerThrSerCysMetThrVal
75808590
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SerCysProArgGlnArgTyrProAlaAsnCysThrValArgAspHis
95100105
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155160165170
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IleAspValLeuLeuIleGlyValGlyTyrValGlyProAlaAspGly
175180185
tcttgtctacatttagctgtggtgtgtgcttcaaaaggagcagggttagaa729
SerLeuTyrIle
190
aaagcccttttgtccgtaggagttgatgtggtgtgagtgaatatatttcta789
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gctaactctggaattttgtttttatgtcctgaaatatatttttctgtga aaaaattaaa909
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ctgccttgaa agtcttttca gctgtgactg caggaagtgg gagtgttttt attgttagct1089
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<211> 221



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 <213> Homo sapiens

<220>  
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       -15                  -10                  -5  
 Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys  
 1                  5                  10                  15  
 Ser Arg Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys  
           20                  25                  30  
 Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val  
       35                  40                  45  
 Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn  
 50                  55                  60  
 Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys  
 65                  70                  75                  80  
 Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr  
           85                  90                  95  
 Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg  
           100                  105                  110  
 Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp  
       115                  120                  125  
 Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp  
       130                  135                  140  
 Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser  
 145                  150                  155                  160  
 Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly  
           165                  170                  175  
 Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile  
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<210> 83  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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<220>  
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 <222> 118..510

<220>  
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 <222> 511..1754

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<220>  
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 <222> 1739..1754

<400> 83

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atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
-20 -15 -10
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Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
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10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
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cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
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atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
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Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
90 95 100 105
ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc 550
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acagacattc gggagacggc cttcgtgttc gccatcactg cggccggcgc cagccacgcc 610
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aaaa 1754

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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..24

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Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro

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75					80						85					
cct	ccc	agg	ccc	ctg	ggg	cag	ccc	tcc	cgc	cgc	agg	ttt	cag	gtc	cca	501
Pro	Pro	Arg	Pro	Leu	Gly	Gln	Pro	Ser	Arg	Arg	Arg	Phe	Gln	Val	Pro	
90				95				100					105			
ggc	ccc	agc	tgacc	gcccc	agcccc	gcgct	gattg	cacct	gtctg	catte						550
Gly	Pro	Ser														
acagacattc	gggagacggc	cttcgtgttc	gccatcactg	cggccggcgc	cagccacgcc											610
gtcacgcagg	cctgttctat	gggcgagctg	ctgcagtgcg	gctgccaggc	gccccgcggg											670
cgggccccctc	cccggccctc	cggcctgccc	ggcacccccg	gacccccctg	ccccgcgggc											730
tccccggaag	gcagcgccgc	ctgggagtg	ggaggctgcg	gcgacgacgt	ggacttcggg											790
gacgagaagt	cgaggctctt	tatggacgcg	cggcacaagc	ggggacgcgg	agacatccgc											850
gcgttggtgc	aactgcacaa	caacgaggcg	ggcaggctgg	ccgtgcggag	ccacacgcgc											910
accgagtgc	aatgccacgg	gctgtcggga	tcatgcgcgc	tgcgcacctg	ctggcagaag											970
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gctcgcacct	gtgggacctc	agggcaccgg	caccggggcg	ctctcgccgc	tcgagcccag											1450
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aaaa																

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<220>  
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Leu	Cys	Pro	Ala	His	Val	Gly	Gly	Leu	Trp	Trp	Ala	Val	Gly	Ser	Pro	
			-5					1			5					
Leu	Val	Met	Asp	Pro	Thr	Ser	Ile	Cys	Arg	Lys	Ala	Arg	Arg	Leu	Ala	
10					15						20					
Gly	Arg	Gln	Ala	Glu	Leu	Cys	Gln	Ala	Glu	Pro	Glu	Val	Val	Ala	Glu	
25				30					35					40		
Leu	Ala	Arg	Gly	Ala	Arg	Leu	Gly	Val	Arg	Glu	Cys	Gln	Phe	Gln	Phe	
			45					50					55			
Arg	Phe	Arg	Arg	Trp	Asn	Cys	Ser	Ser	His	Ser	Lys	Ala	Phe	Gly	Arg	
			60				65					70				
Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	His	Pro	Ala	Arg	Thr	Leu	
75					80						85					
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Gly	Pro	Ser														
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<210> 87  
 <211> 1431  
 <212> DNA  
 <213> Homo sapiens

<220>  
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<220>  
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 <222> 152..655

<220>  
 <221> 3'UTR  
 <222> 656..1431

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<220>  
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 ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172  
 Met Leu Phe Arg Leu Ser Glu  
 1 5  
 cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220  
 His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly  
 10 15 20  
 gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268  
 Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr  
 25 30 35  
 cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316  
 Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln  
 40 45 50 55  
 tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364  
 Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu  
 60 65 70  
 ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412  
 Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu  
 75 80 85  
 gaa gag gag gat gat gaa gaa gag gaa gaa gag gag gac agc cag gct 460  
 Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala  
 90 95 100  
 gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508  
 Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys  
 105 110 115  
 ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556  
 Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu  
 120 125 130 135  
 tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604  
 Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu  
 140 145 150  
 agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652  
 Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly  
 155 160 165  
 aca taggcacca gcctgcatct ccaggagga agtggagggg acatcgctgt 705  
 Thr  
 tccccagaaa ccactctat cctcaccctg ttttgtgtc ttcccctcgc ctgctagggc 765  
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 tccattcacc cagcgggagg tgggatgtga gacagcccac attggaaaat ccagaaaacc 945  
 gggaacaggg atttgccctt cacaattcta ctccccagat cctctcccct ggacacagga 1005

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<210> 88
<211> 168
<212> PRT
<213> Homo sapiens

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<400> 88
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          20          25          30
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          35          40          45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
          50          55          60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65          70          75          80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
          85          90          95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
          100          105          110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
          115          120          125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
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Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145          150          155          160
Pro Ser Pro Ser Glu Pro Gly Thr
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<210> 89
<211> 1431
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..151

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<220>
<221> CDS
<222> 152..655

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<220>
<221> 3'UTR
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<220>
<221> polyA_signal
<222> 1399..1404

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<220>
<221> polyA_site
<222> 1416..1431

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ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172  
Met Leu Phe Arg Leu Ser Glu  
1 5  
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220  
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly  
10 15 20  
gag ggg cac cat ctc aag tgc aag aga ccc aac ccc tgt gcc tac aca 268  
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr  
25 30 35  
cca cct tgc ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316  
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln  
40 45 50 55  
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364  
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu  
60 65 70  
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412  
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu  
75 80 85  
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460  
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala  
90 95 100  
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508  
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys  
105 110 115  
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556  
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu  
120 125 130 135  
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604  
Ser Glu Arg Asp Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu  
140 145 150  
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652  
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly  
155 160 165  
aca taggcacca gctgcatct cccaggagga agtggagggg acatcgctgt 705  
Thr  
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aaaaaa 1431

<210> 90

<211> 168

<212> PRT

<213> Homo sapiens

<400> 90

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Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg  
20 25 30  
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg





				65					70				75				
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Ile	Leu	Glu	Ser	Leu	Asn	Phe	Asn	Leu	Thr	Glu	Ile	Pro	Glu	Ala	Gln		
			80					85					90				
atc	cat	gaa	ggc	ttc	cag	gaa	ctc	ctc	cgt	acc	ctc	aac	cag	cca	gac		440
Ile	His	Glu	Gly	Phe	Gln	Glu	Leu	Leu	Arg	Thr	Leu	Asn	Gln	Pro	Asp		
		95					100					105					
agc	cag	ctc	cag	ctg	acc	acc	ggc	aat	ggc	ctg	ttc	ctc	agc	gag	ggc		488
Ser	Gln	Leu	Gln	Leu	Thr	Thr	Gly	Asn	Gly	Leu	Phe	Leu	Ser	Glu	Gly		
	110						115				120						
ctg	aag	cta	gtg	gat	aag	ttt	ttg	gag	gat	gtt	aaa	aag	ttg	tac	cac		536
Leu	Lys	Leu	Val	Asp	Lys	Phe	Leu	Glu	Asp	Val	Lys	Lys	Leu	Tyr	His		
	125				130					135					140		
tca	gaa	gcc	ttc	act	gtc	aac	ttc	ggg	gac	acc	gaa	gag	gcc	aag	aaa		584
Ser	Glu	Ala	Phe	Thr	Val	Asn	Phe	Gly	Asp	Thr	Glu	Glu	Ala	Lys	Lys		
				145					150					155			
cag	atc	aac	gat	tac	gtg	gag	aag	ggg	act	caa	ggg	aaa	att	gtg	gat		632
Gln	Ile	Asn	Asp	Tyr	Val	Glu	Lys	Gly	Thr	Gln	Gly	Lys	Ile	Val	Asp		
			160					165					170				
ttg	gtc	aag	gag	ctt	gac	aga	gac	aca	gtt	ttt	gct	ctg	gtg	aat	tac		680
Leu	Val	Lys	Glu	Leu	Asp	Arg	Asp	Thr	Val	Phe	Ala	Leu	Val	Asn	Tyr		
		175					180						185				
atc	ttc	ttt	aaa	ggc	aaa	tgg	gag	aga	ccc	ttt	gaa	gtc	aag	gac	acc		728
Ile	Phe	Phe	Lys	Gly	Lys	Trp	Glu	Arg	Pro	Phe	Glu	Val	Lys	Asp	Thr		
	190					195					200						
gag	gaa	gag	gac	ttc	cac	gtg	gac	cag	gcg	acc	acc	gtg	aag	gtg	cct		776
Glu	Glu	Glu	Asp	Phe	His	Val	Asp	Gln	Ala	Thr	Thr	Val	Lys	Val	Pro		
	205				210					215					220		
atg	atg	aag	cgt	tta	ggc	atg	ttt	aac	atc	cag	cac	tgt	aag	aag	ctg		824
Met	Met	Lys	Arg	Leu	Gly	Met	Phe	Asn	Ile	Gln	His	Cys	Lys	Lys	Leu		
				225					230					235			
tcc	agc	tgg	gtg	ctg	ctg	atg	aaa	tac	ctg	ggc	aat	gcc	acc	gcc	atc		872
Ser	Ser	Trp	Val	Leu	Leu	Met	Lys	Tyr	Leu	Gly	Asn	Ala	Thr	Ala	Ile		
			240					245					250				
ttc	ttc	ctg	cct	gat	gag	ggg	aaa	cta	cag	cac	ctg	gaa	aat	gaa	ctc		920
Phe	Phe	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Gln	His	Leu	Glu	Asn	Glu	Leu		
		255					260					265					
acc	cac	gat	atc	atc	acc	aag	ttc	ctg	gaa	aat	gaa	gac	aga	agg	tct		968
Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg	Ser		
	270					275						280					
gcc	agc	tta	cat	tta	ccc	aaa	ctg	tcc	att	act	gga	acc	tat	gat	ctg		1016
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu		
	285				290					295					300		
aag	agc	gtc	ctg	ggg	caa	ctg	ggc	atc	act	aag	gtc	ttc	agc	aat	ggg		1064
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly		
				305				310						315			
gct	gac	ctc	tcc	ggg	gtc	aca	gag	gag	gca	ccc	ctg	aag	ctc	tcc	aag		1112
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys		
		320						325					330				
gcc	gtg	cat	aag	gct	gtg	ctg	acc	atc	gac	gag	aaa	ggg	act	gaa	gct		1160
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala		
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gct	ggg	gcc	atg	ttt	tta	gag	gcc	ata	ccc	atg	tct	atc	ccc	ccc	gag		1208
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro	Glu		
	350				355						360						
gtc	aag	ttc	aac	aaa	ccc	ttt	gtc	ttc	tta	atg	att	gaa	caa	aat	acc		1256
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Glu	Gln	Asn	Thr		
	365				370					375				380			
aag	tct	ccc	ctc	ttc	atg	gga	aaa	gtg	gtg	aat	ccc	acc	caa	aaa			1301
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys			
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 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> 1..24

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                   -5                  1                  5  
 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn  
           10                  15                  20  
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln  
   25                  30                  35                  40  
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser  
                   45                  50                  55  
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr  
                   60                  65                  70  
 His Asp Glu Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro  
           75                  80                  85  
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn  
   90                  95                  100  
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu  
 105                  110                  115                  120  
 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys  
                   125                  130                  135  
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu  
                   140                  145                  150  
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys  
           155                  160                  165  
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu  
   170                  175                  180  
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
 185                  190                  195                  200  
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val  
                   205                  210                  215  
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys  
                   220                  225                  230  
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala  
           235                  240                  245  
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu  
   250                  255                  260  
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp  
 265                  270                  275                  280  
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr  
                   285                  290                  295  
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
           300                  305                  310  
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys  
           315                  320                  325  
 Leu Ser Lys Ala Val His Lys Lys Ala Val Leu Thr Ile Asp Glu Lys Gly  
   330                  335                  340  
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile  
 345                  350                  355                  360  
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu  
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Gln Lys

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<220>  
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<222> 1101..1115

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ctttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180  
ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240  
gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295  
Met His Phe Gly Leu Leu  
-15  
tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343  
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu  
-10 -5 1  
gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391  
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu  
5 10 15 20  
aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439  
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys  
25 30 35  
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487  
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys  
40 45 50  
gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535  
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu  
55 60 65  
agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583  
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg  
70 75 80  
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631  
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu  
85 90 95 100  
gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679  
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr  
105 110 115  
aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727  
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp  
120 125 130  
gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggg 783

Ala Ile  
 ccgaatggtt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843  
 actccgcaat caaccaaggt tcccagcctt tttgttacaa aagaaggaac aaatgatggt 903  
 tggaagaatg cggctcatat ttaccaagtc tttctgaacg ctttctgcat tcatgcatcc 963  
 atgttctttc taggattgga tagcatttca tgcctatggt aatatttgtg cttttggcat 1023  
 ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083  
 atattttacat gcataggaaa aaaaaaaaaa aa 1115

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 <212> PRT  
 <213> Homo sapiens

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 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp  
 1 5 10  
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys  
 15 20 25  
 Ala Asp Asp Ser Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn  
 30 35 40 45  
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly  
 50 55 60  
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr  
 65 70 75  
 Arg Asp Asn Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys  
 80 85 90  
 Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr  
 95 100 105  
 Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys His Val Asn Val Ser  
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 Ser Met Val Asp Ala Trp Ala Ile  
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tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180  
ggaaaaacag aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240  
gattttactt ag atg att tac aca atg aag aaa gta cat gca ctt tgg gct 291  
Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala  
-25 -20 -15  
tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat 339  
Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp  
-10 -5 1  
tct gag gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca 387  
Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro  
5 10 15  
cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat ggc 435  
Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly  
20 25 30  
cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga 483  
Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg  
35 40 45 50  
cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga 531  
Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg  
55 60 65  
ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca 579  
Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala  
70 75 80  
aac agg att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc 627  
Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys  
85 90 95  
ttt ttg gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat 675  
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr  
100 105 110  
ttt tat aac aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga 723  
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly  
115 120 125 130  
tgc ctg ggc aat caa caa ttt tgagacactg gaacaatgca agaacatttg 774  
Cys Leu Gly Asn Gln Gln Phe  
135  
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atggtgtctc actccagcag acagaggatt gtgtcgtgcc aatgagaaca gattctacta 954  
caattcagtc attgggaaat gccgccatt taagtacagt ggatgtgggg gaaatgaaaa 1014  
caattttact tccaacaag aatgtctgag ggcattgtaa aaaggtttca tccaaagaat 1074  
atcaaaagga ggcctaatta aaaccaaag aaaaagaaag aagcagagag tgaaaatagc 1134  
atatgaagaa atttttgtta aaaatatgtg aattttgttat agcaatgtaa cattaattct 1194  
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<212> PRT  
<213> Homo sapiens

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<222> 1..28

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Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu  
-10 -5 1



Arg	Phe	Arg	Arg	Trp	Asn	Cys	Ser	Ser	His	Ser	Lys	Ala	Phe	Gly	Arg		
		60					65					70					
atc	ctg	caa	cag	ggt	cag	tgt	ggg	gag	ggg	gcg	gaa	gtg	ggg	ctg	ctt	453	
Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	Ala	Glu	Val	Gly	Leu	Leu		
		75					80					85					
tct	ccc	tgc	tgt	ggg	acc	cga	gga	gag	gag	aac	tgg	ttc	gct	gaa	gtt	501	
Ser	Pro	Cys	Cys	Gly	Thr	Arg	Gly	Glu	Glu	Asn	Trp	Phe	Ala	Glu	Val		
		90				95				100				105			
gcc	tgagccccac	ttccccctca	catgtgtctg	ggcaccctgc	aaggaccctg											554	
Ala																	
cctcccaggc	ccctggggca	gccctcccgc	cgcaggtttc	aggtcccagg	ccccagctga	614											
ccgccccagc	ccgcgctgat	tgacactgtc	tgcattcaca	gacattcggg	agacggcctt	674											
cgtgttcgcc	atcactgcgg	ccggcgccag	ccacgcgcgc	acgcaggcct	gttctatggg	734											
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cgaggcgggc	aggctggccg	tgcgagagcca	cacgcgcacc	gagtgcacaa	gccacgggct	1034											
gtcgggatca	tgcgcgctgc	gcacctgctg	gcagaagctg	cctccatttc	gcgaggtggg	1094											
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cgggcaccgc	caggagagcg	tgacgctcga	agagaactgc	ctgtgccgct	tcactgggtg	1394											
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caggggcgcca	gacggccccg	aaaaggcgct	cggggagcgt	ttaaaggaca	ctgtacaggc	1694											
cctccctccc	cttgccctct	aggaggaaac	agtttttttag	actggaaaaa	agccagtcta	1754											
aaggcctctg	gatactgggc	tccccagaac	tgctggccac	aggatggtgg	gtgaggttag	1814											
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 <212> PRT  
 <213> Homo sapiens

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Leu	Cys	Pro	Ala	His	Val	Gly	Gly	Leu	Trp	Trp	Ala	Val	Gly	Ser	Pro		
			-5					1				5					
Leu	Val	Met	Asp	Pro	Thr	Ser	Ile	Cys	Arg	Lys	Ala	Arg	Arg	Leu	Ala		
		10				15					20						
Gly	Arg	Gln	Ala	Glu	Leu	Cys	Gln	Ala	Glu	Pro	Glu	Val	Val	Ala	Glu		
		25			30					35				40			
Leu	Ala	Arg	Gly	Ala	Arg	Leu	Gly	Val	Arg	Glu	Cys	Gln	Phe	Gln	Phe		
			45					50						55			
Arg	Phe	Arg	Arg	Trp	Asn	Cys	Ser	Ser	His	Ser	Lys	Ala	Phe	Gly	Arg		
			60					65					70				
Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	Ala	Glu	Val	Gly	Leu	Leu		
		75					80					85					
Ser	Pro	Cys	Cys	Gly	Thr	Arg	Gly	Glu	Glu	Asn	Trp	Phe	Ala	Glu	Val		
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Ala																	
105																	

<210> 99

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 <212> DNA  
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<220>  
 <221> 3'UTR  
 <222> 614..667

<220>  
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<220>  
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 Met Ile Val Lys Gly Val Ala  
 1 5  
 tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163  
 Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser  
 10 15 20  
 tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211  
 Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val  
 25 30 35  
 gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259  
 Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile  
 40 45 50 55  
 ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307  
 Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys  
 60 65 70  
 acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355  
 Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile  
 75 80 85  
 aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403  
 Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr  
 90 95 100  
 gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451  
 Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu  
 105 110 115  
 tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499  
 Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met  
 120 125 130 135  
 gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547  
 Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val  
 140 145 150  
 gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595  
 Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys  
 155 160 165  
 caa acc act gtg aaa aat tagctttgaa agctatatct ggaataaata 643  
 Gln Thr Thr Val Lys Asn  
 170  
 tctttcgcaa aaaaaaaaaa aaaa 667



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 <213> Homo sapiens

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 Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn  
 35 40 45  
 Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val  
 50 55 60  
 Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile  
 65 70 75 80  
 His Gly Tyr Ala Phe Ala Ile Thr Asn Asn Gly Tyr Ile Leu Thr His  
 85 90 95  
 Pro Glu Leu Arg Leu Leu Tyr Glu Glu Gly Lys Lys Arg Arg Lys Pro  
 100 105 110  
 Asn Tyr Ser Ser Val Asp Leu Ser Glu Val Glu Trp Glu Asp Arg Asp  
 115 120 125  
 Asp Val Leu Arg Asn Ala Met Val Asn Arg Lys Thr Gly Lys Phe Ser  
 130 135 140  
 Met Glu Val Lys Lys Thr Val Asp Lys Gly Val His Phe Ser Gln Thr  
 145 150 155 160  
 Phe Leu Leu Leu Asn Leu Lys Gln Thr Thr Val Lys Asn  
 165 170

<210> 101  
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 <212> DNA  
 <213> Homo sapiens

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<220>  
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<220>  
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 <222> 640..1062

<220>  
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<220>  
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 <222> 1047..1062

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 gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg 174  
 Met Ala Cys Trp Pro Gln Leu  
 1 5  
 agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt 222  
 Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys

10	15	20	
cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg			270
Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu			
25	30	35	
atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat			318
Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His			
40	45	50	55
ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag			366
Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln			
60	65	70	
ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct			414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro			
75	80	85	
ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct			462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala			
90	95	100	
cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac			510
Arg Leu Phe Ser Asp Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp			
105	110	115	
acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc			558
Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile			
120	125	130	135
aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag			606
Lys Lys Ser Ser Ser Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln			
140	145	150	
aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtcct cattgtcagg			659
Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu			
155	160		
cctctaagcc caagccaagc catcgcatcc cctgtgactt gcacatatatac gcccagatgg			719
cctgaagtaa ctgaagaatc acaaaaagaag tgaaaaaggcc ctgcctcgcc ttaactgatg			779
acgttccacc attgtgattt gttcctgccc caccttaact gagtgattaa ccctgtgaat			839
ttccttctcc tggctcagaa gctccccac tgagcacctt gtgacccctt gcccctgccc			899
accagagaac aacccccctt gactgtaatt ttccattacc ttcccaaatac ctataaaaacg			959
gccccacccc tatctccctt tgctgactct cttttcggac tcagcccacc tgcagccagg			1019
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<211> 162

<212> PRT

<213> Homo sapiens

<400> 102

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20	25
Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro	30
35	40
Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala	45
50	55
Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro	60
65	70
Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn	75
85	90
Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu	95
100	105
Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val	110
115	120
Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys	125
130	135
Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala	140
145	150
Leu Leu	155
	160

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 ggaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120  
 cagatgtgta cggatgaaaa tacagtgcag atg agt cag aaa ccg gcc aag gag 173  
 Met Ser Gln Lys Pro Ala Lys Glu  
 1 5  
 ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221  
 Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile  
 10 15 20  
 cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269  
 His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val  
 25 30 35 40  
 gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317  
 Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys  
 45 50 55  
 gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365  
 Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg  
 60 65 70  
 aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412  
 Lys Ile Arg Pro Thr Pro Lys Lys Lys  
 75 80  
 ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac ccctggatga 472  
 agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532  
 gctcatgggc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592  
 tcatcccatt gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652  
 atccttcacac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712  
 tggaaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772  
 gcgtgggtggc gggcgccctgt ggtcccagct actcgggagg ctgagggcagg agaatggcgt 832  
 gaacctggga ggcggagctt gcagtgcac gagatcgac cactgcactc cagcctgggc 892  
 gacagagcga gactctgtct caaacaacaa aaaaaaaaaa a 933

<210> 104  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
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 1 5 10 15  
 Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe  
 20 25 30



120	125	130	
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg			535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg			
135	140	145	
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat			583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn			
150	155	160	165
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa			631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu			
170	175	180	
tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt			679
Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe			
185	190	195	
gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gcc aca			727
Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr			
200	205	210	
ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa			775
Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu			
215	220	225	
tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct			823
Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser			
230	235	240	245
tgt aaa gta cct gtg aaa gcc act gtg gtg tac caa gga gag aga			871
Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg			
250	255	260	
gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa			919
Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys			
265	270	275	
gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag			967
Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu			
280	285	290	
gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag			1015
Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys			
295	300	305	
gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag			1063
Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys			
310	315	320	325
cca tgc taagggtggtt ttcagattcc acataaaatg tcacacttgt ttcttggtca			1119
Pro Cys			
tccaaggaac ctaattgaaa tttaaaaata aagctactga atttattgcc gcaaaaaaaaa			1179
aaaaaaaa			1187

<210> 106  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..19

<400> 106  
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 Ala Ile Ala Gly Arg Thr Cys Pro Lys Pro Asp Asp Leu Pro Phe Ser  
 Thr Val Val Pro Leu Lys Thr Phe Tyr Glu Pro Gly Glu Glu Ile Thr  
 Tyr Ser Cys Lys Pro Gly Tyr Val Ser Arg Gly Gly Met Arg Lys Phe  
 Ile Cys Pro Leu Thr Gly Leu Trp Leu Ile Asn Thr Leu Lys Cys Thr  
 Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg



agc tgc aaa agc gat gcc gat tct ggt ttc ctg ggg ctg cgg ccc act	99
Ser Ser Lys Ser Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr	
15 20 25	
tcg gtg gac cca gcg ctg agg cgg cgg cgg cga ggc cca aga aat aag	147
Ser Val Asp Pro Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys	
30 35 40	
aag cgg ggc tgg cgg cgg ctt gct cag gag ccg ctg ggg ctg gag gtt	195
Lys Arg Gly Trp Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val	
45 50 55 60	
gac cag ttc ctg gaa gac gtg cgg cta cag gag cgc acg agc ggt ggc	243
Asp Gln Phe Leu Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly	
65 70 75	
ttg ttg tca gag gcc cca aat gaa aaa ctc ttc ttc gtg gac act ggc	291
Leu Leu Ser Glu Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly	
80 85 90	
tcc aag gaa aaa ggg ctg aca aag aag aga acc aaa gtc cag aag aag	339
Ser Lys Glu Lys Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys	
95 100 105	
tca ctg ctt ctc aag aaa ccc ctt cgg gtt gac ctc atc ctc gag aac	387
Ser Leu Leu Leu Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn	
110 115 120	
aca tcc aaa gtc cct gcc ccc aaa gac gtc ctc gcc cac cag gtc ccc	435
Thr Ser Lys Val Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro	
125 130 135 140	
aac gcc aag aag ctc agg cgg aag gag cag cta tgg gag aag ctg gcc	483
Asn Ala Lys Lys Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala	
145 150 155	
aag cag ggc gag ctg ccc cgg gag gtg cgc agg gcc cag gcc cgg ctc	531
Lys Gln Gly Glu Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu	
160 165 170	
ctc aac cct tct gca aca agg gcc aag ccc ggg ccc cag gac acc gta	579
Leu Asn Pro Ser Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val	
175 180 185	
gag cgg ccc ttc tac gac ctc tgg gcc tca gac aac ccc ctg gac agg	627
Glu Arg Pro Phe Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg	
190 195 200	
ccg ttg gtt ggc cag gat gag ttt ttc ctg gag cag acc aag aag aaa	675
Pro Leu Val Gly Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys	
205 210 215 220	
gga gtg aag cgg cca gca cgc ctg cac acc aag ccg tcc cag gca ccc	723
Gly Val Lys Arg Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro	
225 230 235	
gcc gtg gag gtg gcg cct gcc gga gct tcc tac aat cca tcc ttt gaa	771
Ala Val Glu Val Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu	
240 245 250	
gac cac cag acc ctg ctc tca gcg gcc cac gag gtg gag ttg cag cgg	819
Asp His Gln Thr Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg	
255 260 265	
cag aag gag gcg gag aag ctg gag cgg cag ctg gcc ctg ccc gcc acg	867
Gln Lys Glu Ala Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr	
270 275 280	
gag cag gcc gcc acc cag gag tcc aca ttc cag gag ctg tgc gag ggg	915
Glu Gln Ala Ala Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly	
285 290 295 300	
ctg ctg gag gag tgc gat ggt gag ggg gag cca ggc cag ggc gag ggg	963
Leu Leu Glu Glu Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly	
305 310 315	
ccg gag gct ggg gat gcc gag gtc tgt ccc acg ccc gcc cgc ctg gcc	1011
Pro Glu Ala Gly Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala	
320 325 330	
acc aca gag aag aag acg gag cag cag cgg cgg cgg gag aag gct gtg	1059
Thr Thr Glu Lys Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val	
335 340 345	

cac agg ctg cgg gta cag cag gcc gcg ttg cgg gcc gcc cgg ctc cgg 1107  
 His Arg Leu Arg Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg  
 350 355 360  
 cac cag gag ctg ttc cgg ctg cgc ggg atc aag gcc cag gtg gcc ctg 1155  
 His Gln Glu Leu Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu  
 365 370 375 380  
 agg ctg gcg gag ctg gcg cgg cgg cag agg cgg cgg cag gcg cgg cgg 1203  
 Arg Leu Ala Glu Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg  
 385 390 395  
 gag gct gag gct gac aag ccc cga agg ctg ggg cgg ctc aag tac cag 1251  
 Glu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln  
 400 405 410  
 gca cct gac atc gac gtg cag ctg agc tcg gag ctg aca gac tcg ctc 1299  
 Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu  
 415 420 425  
 agg acc ctg aag ccc gag ggc aac atc ctt cga gac cgg ttc aag agc 1347  
 Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser  
 430 435 440  
 ttc cag agg agg aat atg atc gag cct cga gag aga gcc aag ttc aaa 1395  
 Phe Gln Arg Arg Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys  
 445 450 455 460  
 cgc aag tac aag gtg aag ctg gtg gag aag cgg gcg ttc cgt gag atc 1443  
 Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile  
 465 470 475  
 cag ttg tagctgccat cagatgccgg agactcgccc ttcaataaaaa aatctcttct 1499  
 Gln Leu  
 agctcaaaaa aaaaaaaaaa a 1520

<210> 108

<211> 478

<212> PRT

<213> Homo sapiens

<400> 108

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 Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro  
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 Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp  
 35 40 45  
 Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu  
 50 55 60  
 Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu  
 65 70 75 80  
 Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys  
 85 90 95  
 Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu  
 100 105 110  
 Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val  
 115 120 125  
 Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys  
 130 135 140  
 Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu  
 145 150 155 160  
 Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser  
 165 170 175  
 Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe  
 180 185 190  
 Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly  
 195 200 205  
 Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg  
 210 215 220  
 Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val



225					230					235				240	
Ala	Pro	Ala	Gly	Ala	Ser	Tyr	Asn	Pro	Ser	Phe	Glu	Asp	His	Gln	Thr
				245					250					255	
Leu	Leu	Ser	Ala	Ala	His	Glu	Val	Glu	Leu	Gln	Arg	Gln	Lys	Glu	Ala
			260					265					270		
Glu	Lys	Leu	Glu	Arg	Gln	Leu	Ala	Leu	Pro	Ala	Thr	Glu	Gln	Ala	Ala
			275				280					285			
Thr	Gln	Glu	Ser	Thr	Phe	Gln	Glu	Leu	Cys	Glu	Gly	Leu	Leu	Glu	Glu
			290			295					300				
Ser	Asp	Gly	Glu	Gly	Glu	Pro	Gly	Gln	Gly	Glu	Gly	Pro	Glu	Ala	Gly
305					310					315				320	
Asp	Ala	Glu	Val	Cys	Pro	Thr	Pro	Ala	Arg	Leu	Ala	Thr	Thr	Glu	Lys
				325					330					335	
Lys	Thr	Glu	Gln	Gln	Arg	Arg	Arg	Glu	Lys	Ala	Val	His	Arg	Leu	Arg
			340				345					350			
Val	Gln	Gln	Ala	Ala	Leu	Arg	Ala	Ala	Arg	Leu	Arg	His	Gln	Glu	Leu
			355				360					365			
Phe	Arg	Leu	Arg	Gly	Ile	Lys	Ala	Gln	Val	Ala	Leu	Arg	Leu	Ala	Glu
370					375					380					
Leu	Ala	Arg	Arg	Gln	Arg	Arg	Gln	Ala	Arg	Arg	Glu	Ala	Glu	Ala	
385					390				395					400	
Asp	Lys	Pro	Arg	Arg	Leu	Gly	Arg	Leu	Lys	Tyr	Gln	Ala	Pro	Asp	Ile
				405					410					415	
Asp	Val	Gln	Leu	Ser	Ser	Glu	Leu	Thr	Asp	Ser	Leu	Arg	Thr	Leu	Lys
			420					425					430		
Pro	Glu	Gly	Asn	Ile	Leu	Arg	Asp	Arg	Phe	Lys	Ser	Phe	Gln	Arg	Arg
			435				440					445			
Asn	Met	Ile	Glu	Pro	Arg	Glu	Arg	Ala	Lys	Phe	Lys	Arg	Lys	Tyr	Lys
	450				455					460					
Val	Lys	Leu	Val	Glu	Lys	Arg	Ala	Phe	Arg	Glu	Ile	Gln	Leu		
465					470					475					

<210> 109  
 <211> 1789  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..94

<220>  
 <221> CDS  
 <222> 95..1252

<220>  
 <221> 3'UTR  
 <222> 1253..1789

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<220>  
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 <222> 1774..1789

<400> 109  
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 Met Cys Leu Leu Leu Ser Cys  
 -10  
 cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163

Pro	Cys	His	Pro	Ser	Ala	His	Gly	Gln	Ser	Met	Trp	Ile	Glu	Arg	Thr	
		-5					1				5					
tcc	ttc	gtg	act	gca	tac	aag	ctg	ccg	ggg	atc	ctg	cgc	tgg	ttt	gag	211
Ser	Phe	Val	Thr	Ala	Tyr	Lys	Leu	Pro	Gly	Ile	Leu	Arg	Trp	Phe	Glu	
10				15					20					25		
gtg	gtg	cac	atg	tcg	cag	acc	aca	att	agt	cct	ctg	gag	aat	gcc	ata	259
Val	Val	His	Met	Ser	Gln	Thr	Thr	Ile	Ser	Pro	Leu	Glu	Asn	Ala	Ile	
			30						35					40		
gaa	acc	atg	tcc	acg	gcc	aat	gag	aag	atc	ctg	atg	atg	ata	aac	cag	307
Glu	Thr	Met	Ser	Thr	Ala	Asn	Glu	Lys	Ile	Leu	Met	Met	Ile	Asn	Gln	
			45					50					55			
tac	cag	agt	gat	gag	acc	ctc	ccc	atc	aac	cca	ctc	tcc	atg	ctc	ctg	355
Tyr	Gln	Ser	Asp	Glu	Thr	Leu	Pro	Ile	Asn	Pro	Leu	Ser	Met	Leu	Leu	
		60					65					70				
aac	ggg	att	gtg	gac	cct	gct	gtc	atg	gga	ggc	ttc	gcc	aag	tat	gag	403
Asn	Gly	Ile	Val	Asp	Pro	Ala	Val	Met	Gly	Gly	Phe	Ala	Lys	Tyr	Glu	
75						80					85					
aag	gcc	ttc	ttc	act	gaa	gag	tat	gtc	agg	gac	cac	cct	gag	gac	cag	451
Lys	Ala	Phe	Phe	Thr	Glu	Glu	Tyr	Val	Arg	Asp	His	Pro	Glu	Asp	Gln	
90				95					100					105		
gac	aag	ctg	acc	cac	ctc	aag	gac	ctg	att	gca	tgg	cag	atc	ccc	ttc	499
Asp	Lys	Leu	Thr	His	Leu	Lys	Asp	Leu	Ile	Ala	Trp	Gln	Ile	Pro	Phe	
				110					115					120		
ttg	gga	gct	ggg	att	aag	atc	cat	gag	aaa	agg	gtg	tca	gat	aac	ttg	547
Leu	Gly	Ala	Gly	Ile	Lys	Ile	His	Glu	Lys	Arg	Val	Ser	Asp	Asn	Leu	
			125					130					135			
cga	ccc	ttc	cat	gac	cgg	atg	gag	gaa	tgt	ttc	aag	aac	ctg	aaa	atg	595
Arg	Pro	Phe	His	Asp	Arg	Met	Glu	Glu	Cys	Phe	Lys	Asn	Leu	Lys	Met	
		140					145				150					
aag	gtg	gag	aag	gag	tac	ggt	gtc	cga	gag	atg	cct	gac	ttt	gac	gac	643
Lys	Val	Glu	Lys	Glu	Tyr	Gly	Val	Arg	Glu	Met	Pro	Asp	Phe	Asp	Asp	
155						160					165					
agg	aga	gtg	ggc	cgt	ccc	agg	tct	atg	ctg	cgc	tca	tac	aga	cag	atg	691
Arg	Arg	Val	Gly	Arg	Pro	Arg	Ser	Met	Leu	Arg	Ser	Tyr	Arg	Gln	Met	
170					175					180				185		
tcc	atc	atc	tct	ctg	gct	tcc	atg	aat	tct	gac	tgc	agc	acc	ccc	agc	739
Ser	Ile	Ile	Ser	Leu	Ala	Ser	Met	Asn	Ser	Asp	Cys	Ser	Thr	Pro	Ser	
				190					195					200		
aag	cct	acc	tca	gag	agc	ttt	gac	ctg	gaa	tta	gca	tca	ccc	aag	acg	787
Lys	Pro	Thr	Ser	Glu	Ser	Phe	Asp	Leu	Glu	Leu	Ala	Ser	Pro	Lys	Thr	
			205					210					215			
ccg	aga	gtg	gag	cag	gag	gaa	ccg	atc	tcc	ccg	ggg	agc	acc	ctg	cct	835
Pro	Arg	Val	Glu	Gln	Glu	Glu	Pro	Ile	Ser	Pro	Gly	Ser	Thr	Leu	Pro	
		220				225						230				
gag	gtc	aag	ctg	cgg	agg	tcc	aag	aag	agg	aca	aag	aga	agc	agc	gta	883
Glu	Val	Lys	Leu	Arg	Arg	Ser	Lys	Lys	Arg	Thr	Lys	Arg	Ser	Ser	Val	
		235				240					245					
gtt	ttt	gcg	gat	gag	aaa	gca	gct	gca	gag	tcg	gac	ctg	aag	cgg	ctt	931
Val	Phe	Ala	Asp	Glu	Lys	Ala	Ala	Ala	Glu	Ser	Asp	Leu	Lys	Arg	Leu	
250					255					260				265		
tcc	agg	aag	cat	gag	ttc	atg	agt	gac	acc	aac	ctc	tcg	gag	cat	gcg	979
Ser	Arg	Lys	His	Glu	Phe	Met	Ser	Asp	Thr	Asn	Leu	Ser	Glu	His	Ala	
				270					275					280		
gcc	atc	ccc	ctc	aag	gcg	tct	gtc	ctc	tct	caa	atg	agc	ttt	gcc	agc	1027
Ala	Ile	Pro	Leu	Lys	Ala	Ser	Val	Leu	Ser	Gln	Met	Ser	Phe	Ala	Ser	
				285				290					295			
cag	tcc	atg	cct	acc	atc	cca	gcc	ctg	gcg	ctc	tca	gtg	gca	ggc	atc	1075
Gln	Ser	Met	Pro	Thr	Ile	Pro	Ala	Leu	Ala	Leu	Ser	Val	Ala	Gly	Ile	
		300					305					310				
cct	ggg	ttg	gat	gag	gcc	aac	aca	tct	ccc	cgc	ctc	agc	cag	acc	ttc	1123
Pro	Gly	Leu	Asp	Glu	Ala	Asn	Thr	Ser	Pro	Arg	Leu	Ser	Gln	Thr	Phe	
		315				320					325					
ctc	caa	ctc	tca	gat	ggt	gac	aag	aag	aca	ctc	aca	cgg	aag	aag	gtc	1171

Leu Gln Leu Ser Asp Gly Asp Lys Lys Thr Leu Thr Arg Lys Lys Val  
 330 335 340 345  
 aat cag ttc ttc aag aca atg ctg gcc agc aaa tcg gct gaa gaa ggc 1219  
 Asn Gln Phe Phe Lys Thr Met Leu Ala Ser Lys Ser Ala Glu Glu Gly  
 350 355 360  
 aaa cag atc cca gac tcg ctg tcc acg gac ctg tgagctgctg ctgactaggg 1272  
 Lys Gln Ile Pro Asp Ser Leu Ser Thr Asp Leu  
 365 370  
 ctgcatggga gagccagggg ggggagtttc tggaagagga aagccatgcg tggaacatcg 1332  
 aagcctcaga gagggggaga ctgtcccat cagttgtcct tacttagagg agacagagag 1392  
 gccaatcagg tcccagagct tgaatgctaa caagcccagc atcccctggg gctgtgatca 1452  
 tgggtggatga ggaagcctca acgtagattc ctgaactcaa ggtaccagca agaatgcctt 1512  
 ctcccagtgt gctctcccca acatcctagg cacagctttc ataaccagc ttcttaggtg 1572  
 taagaaaactg tttttatctc atttattaag tctcagaact taacagaaaa ggaagccttt 1632  
 taaatattct ttttaatttt attttagatt aacagttttg tactttacat ttttttatac 1692  
 aaccaaccag tttcttttct agccaatcat ctctgaagag ttgctgtttc ttactgacaa 1752  
 taaaaaatgt tctcttggtt caaaaaaaaa aaaaaaa 1789

<210> 110  
 <211> 386  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..15

<400> 110  
 Met Cys Leu Leu Leu Ser Cys Pro Cys His Pro Ser Ala His Gly Gln  
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 Ser Met Trp Ile Glu Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro  
 5 10 15  
 Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile  
 20 25 30  
 Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys  
 35 40 45  
 Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile  
 50 55 60 65  
 Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met  
 70 75 80  
 Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val  
 85 90 95  
 Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu  
 100 105 110  
 Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu  
 115 120 125  
 Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu  
 130 135 140 145  
 Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg  
 150 155 160  
 Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met  
 165 170 175  
 Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn  
 180 185 190  
 Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu  
 195 200 205  
 Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile  
 210 215 220 225  
 Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys  
 230 235 240  
 Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala  
 245 250 255  
 Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp

260	265	270
Thr Asn Leu Ser Glu His	Ala Ala Ile Pro Leu Lys	Ala Ser Val Leu
275	280	285
Ser Gln Met Ser Phe Ala	Ser Gln Ser Met Pro Thr	Ile Pro Ala Leu
290	295	300
Ala Leu Ser Val Ala Gly	Ile Pro Gly Leu Asp	Glu Ala Asn Thr Ser
310	315	320
Pro Arg Leu Ser Gln Thr	Phe Leu Gln Leu Ser	Asp Gly Asp Lys Lys
325	330	335
Thr Leu Thr Arg Lys Lys	Val Asn Gln Phe Phe	Lys Thr Met Leu Ala
340	345	350
Ser Lys Ser Ala Glu Glu	Gly Lys Gln Ile Pro	Asp Ser Leu Ser Thr
355	360	365
Asp Leu		
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 Met Ser Thr Phe  
 1  
 ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162  
 Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys  
 5 10 15 20  
 ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc 210  
 Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser  
 25 30 35  
 tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258  
 Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu  
 40 45 50  
 tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306  
 Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met  
 55 60 65  
 tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354  
 Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala  
 70 75 80  
 gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402  
 Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys

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tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa	450						
Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu							
		105		110		115	
aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc	498						
Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu							
		120		125		130	
tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct	546						
Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala							
		135		140		145	
tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg	594						
Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val							
		150		155		160	
atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt	642						
Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu							
		165		170		175	
ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act	690						
Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn Phe Phe Gly Thr							
		185		190		195	
gtg gag gtc aca aag acg ttt ttg cct ctt ctt aga aaa tcc aaa ggg	738						
Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly							
		200		205		210	
agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtg gaa agg	786						
Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg							
		215		220		225	
ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca	834						
Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser							
		230		235		240	
gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc	882						
Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile							
		245		250		255	
caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg	930						
Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp							
		265		270		275	
gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag	978						
Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln							
		280		285		290	
gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta	1026						
Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg Asn Phe Leu Leu							
		295		300		305	
ttg atc aac tcg tta gcc agc aag gac ttc tct ccg gtg ctg cgg gac	1074						
Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro Val Leu Arg Asp							
		310		315		320	
atc cag cat gct atc ttg gcg aag agc cct ttt gcc tat tac acg cca	1122						
Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala Tyr Tyr Thr Pro							
		325		330		335	
ggg aaa ggc gct tac ttg tgg atc tgc ctt gct cac tat ttg cct att	1170						
Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His Tyr Leu Pro Ile							
		345		350		355	
ggc ata tat gat tac ttt gct aaa aga cat ttt ggc caa gac aag ccc	1218						
Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly Gln Asp Lys Pro							
		360		365		370	
atg ccc aga gct tta aga atg cct aac tac aag aaa aag gcc ccc	1263						
Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys Lys Ala Pro							
		375		380		385	
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aaaaaaaaaaga aaaaaaaaaa aaaaaa	1408						

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 <212> PRT  
 <213> Homo sapiens

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Gln Leu Trp Ser Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys  
35 40 45  
Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser  
50 55 60  
Cys Phe Leu Met Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val  
65 70 75 80  
Asp Gln Lys Ala Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His  
85 90 95  
Ala Leu Cys Lys Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly  
100 105 110  
Val Leu Asn Glu Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys  
115 120 125  
Ser Pro Arg Leu Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln  
130 135 140  
Ile Lys Asp Ala Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly  
145 150 155 160  
Leu Trp Ala Val Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp  
165 170 175  
Gly Glu Leu Leu Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn  
180 185 190  
Phe Phe Gly Thr Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg  
195 200 205  
Lys Ser Lys Gly Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala  
210 215 220  
Pro Val Glu Arg Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr  
225 230 235 240  
Met Phe Ser Ser Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys  
245 250 255  
Val Ala Ser Ile Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr  
260 265 270  
Ser Asp Lys Trp Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro  
275 280 285  
Ala Glu Val Gln Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg  
290 295 300  
Asn Phe Leu Leu Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro  
305 310 315 320  
Val Leu Arg Asp Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala  
325 330 335  
Tyr Tyr Thr Pro Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His  
340 345 350  
Tyr Leu Pro Ile Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly  
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370 375 380  
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 tgggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggcccg aggccagtcc 180  
 aacccttggg gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240  
 cggcccgcag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300  
 agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356  
 Met Gly Arg Thr  
 cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404  
 Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala  
 -15 -10 -5 1  
 tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452  
 Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys  
 5 10 15  
 atc tgg gac gaa gac gag gag tct acg gac acc tca tagattgggg 498  
 Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser  
 20 25  
 ttgagactgt gaaaggagct aaaactaacg ctggggcagg gtctggggcc aaacttcagg 558  
 gtgattcaga ggtcaagcct gaggtgagtt tgggactcga ggattgtccg ggtgtaaaag 618  
 agaaggccca ttcaggatcc cacagcggag gtggcctaga ggccaaggcc aaggcccttt 678  
 tcaacacgct gaaggaacag gcaagtgcaa aggcaggcaa aggggctagg gtgggtacca 738  
 tctctgggaa caggaccctt gcaccgagtt taccctgccc agggaggcagg ggtggaggct 798  
 gccacccac caggagtgga tctagggccg ggggcagggc aagtggaaaa tccaagggaa 858  
 agggccgaag taagagcacc agggctccag ctacaacatg gcctgtcccg agaggcaagt 918  
 tcaactttcc ttataaaatt gatgatattc tgagtgtccc cgacctccaa aaggctcctca 978  
 acatcctgga gcgaacaaat gatcctttta ttcaagaagt agccttggtc actctgggta 1038  
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 ttgcaaaaaa aaaaaaaaaa 1118

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 <212> PRT  
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<220>  
 <221> SIGNAL  
 <222> 1..20

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 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser  
 15 20 25